

```

1 ATGTCCAGCG CTCGGACCCC CCTACCCACG CTGAACGAGA GGGACACGGA
51 GCAGCCCACC TTGGGACACC TTGACTCCAA GCCCAGCAGT AAGTCCAACA
101 TGATTCGGGG CCGCAACTCA GCCACCTCTG CTGATGAGCA GCCCCACATT
151 GGAAACTACC GGCTCCTCAA GACCATTGGC AAGGGTAATT TTGCCAAGGT
201 GAAGTTGGCC CGACACATCC TGAAGTTGGC AGAGGTAGCT GTGAAGATCA
251 TTGACAAGAC TCAACTGAAC TCCTCCAGCC TCCAGAACT ATTCCGCGAA
301 GTAAGAATAA TGAAGGTTTT GAATCATCCC AACATAGTTA AATTATTTGA
351 AGTGATTGAG ACTGAGAAAA CGCTCTACCT TGTATGAGG TACGCTAGTG
401 GCGGAGAGGT ATTTGATTAC CTAGTGGCTC ATGGCAGGAT GAAAGAAAAA
451 GAGGCTCGAG CCAAATTCCG CCAGGTAGTG TCTGCTGTGC AGTACTGTCA
501 CCAGAAGTTT ATTGTCCATA GAGACTTAAA GGCAGAAAAC CTGCTCTTGG
551 ATGCTGATAT GAACATCAAG ATTGCAGACT TTGGCTTCAG CAATGAATTC
601 ACCTTTGGGA ACAAGCTGGA CACCTTCTGT GGCAGTCCCC CTTATGCTGC
651 CCCAGAACTC TTCCAGGGCA AAAAATATGA TGGACCCGAG GTGGATGTGT
701 GGAGCCTAGG AGTTATCCTC TATACACTGG TCAGCGGATC CCTGCCTTTT
751 GATGGACAGA ACCTCAAGGA GCTGCGGGAA CGGGTACTGA GGGGAAAATA
801 CCGTATTCCA TTCTACATGT CCACGGACTG TGAAAACCTG CTTAAGAAAT
851 TTCTCATTCT TAATCCCAGC AAGAGAGGCA CTTTAGAGCA AATCATGAAA
901 GATCGATGGA TGAATGTGGG TCACGAAGAT GATGAACTAA AGCCTTACGT
951 GGAGCCACTC CCTGACTACA AGGACCCCCG GCGGACAGAG CTGATGGTGT
1001 CCATGGGTTA TACACGGGAA GAGATCCAGG ACTCGCTGGT GGGCCAGAGA
1051 TACAACGAGG TGATGGCCAC CTATCTGCTC CTGGGCTACA AGAGCTCCGA
1101 GCTGGAAGGC GACACCATCA CCCTGAAACC CCGGCCTTCA GCTGATCTGA
1151 CCAATAGCAG CGCCCCATCC CCATCCCACA AGGTACAGCG CAGCGTGTGC
1201 GCCAATCCCA AGCAGCGGCG CTTACGCGAC CAGGCTGGTC CTGCCATTCC
1251 CACCTCTAAT TCTTACTCTA AGAAGACTCA GAGTAACAAC GCAGAAAATA
1301 AGCGGCCTGA GGAGGACCGG GAGTCAGGGC GGAAAGCCAG CAGCACAGCC
1351 AAGGTGCCTG CCAGCCCCCT GCCCGGTCTG GAGAGGAAGA AGACCACCCC
1401 AACCCCTCC ACGAACAGCG TCCTCTCCAC CAGCACAAT CGAAGCAGGA
1451 ATTCCCCACT TTTGGAGCGG GCCAGCCTCG GCCAGGCCTC CATCCAGAAT
1501 GGCAAAGACA GCACAGCCCC CCAGCGTGTC CCTGTTGCCT CCCCATCCGC
1551 CCACAACATC AGCAGCAGTG GTGGAGCCCC AGACCGAACT AACTTCCCCC
1601 GGGGTGTGTC CAGCCGAAGC ACCTTCCATG CTGGGCAGCT CCGACAGGTG
1651 CGGGACCAGC AGAATTTGCC CTACGGTGTG ACCCCAGCCT CTCCCTCTGG
1701 CCACAGCCAG GGCCGGCGGG GGGCCTCTGG GAGCATCTTC AGCAAGTTCA
1751 CCTCCAAGTT TGTACGCAGG AACCTGAATG AACCTGAAAG CAAAGACCGA
1801 GTGGAGACGC TCAGACCTCA CGTGGTGGGC AGTGGCGGCA ACGACAAAGA
1851 AAAGGAAGAA TTTCGGGAGG CCAAGCCCCG CTCCCTCCGC TTCACGTGGA
1901 GTATGAAGAC CACGAGCTCC ATGGAGCCCA ACGAGATGAT GCGGGAGATC
1951 CGCAAGGTGC TGGACGCGAA CAGCTGCCAG AGCGAGCTGC ATGAGAAGTA
2001 CATGCTGCTG TGCATGCACG GCACGCCGGG CCACGAGGAC TTCGTGCAGT
2051 GGGAGATGGA GGTGTGAAA CTGCCGCGC TCTCTCTCAA CGGGGTTCTGA
2101 TTTAAGCGGA TATCGGGCAC CTCCATGGCC TTCAAAAACA TTGCCTCCAA
2151 AATAGCCAAC GAGCTGAAGC TTAA (SEQ ID NO:1)

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FIGURE 1A

FEATURES:

Start Codon: 1

Stop Codon: 2173

Homologous proteins:

Top 10 BLAST Hits

	Score	E
CRA 18000005076710 /altid=gi 11067437 /def=ref NP_067731.1 ser...	1418	0.0
CRA 46000103792917 /altid=gi 15042611 /def=gb AAK82368.1 AF3876...	1384	0.0
CRA 117000066864950 /altid=gi 9845489 /def=ref NP_004945.2 ELK...	1379	0.0
CRA 18000005061736 /altid=gi 9845487 /def=ref NP_059672.1 ELKL...	1339	0.0
CRA 88000001156998 /altid=gi 7446398 /def=pir G01025 serine/th...	1339	0.0
CRA 149000126080096 /altid=gi 14250622 /def=gb AAH08771.1 AAH08...	1332	0.0
CRA 18000004939026 /altid=gi 6679643 /def=ref NP_031954.1 ELKL...	1319	0.0
CRA 18000004906726 /altid=gi 346945 /def=pir S31333 protein ki...	1248	0.0
CRA 32000237666055 /altid=gi 14764243 /def=ref XP_037764.1 ELK...	875	0.0
CRA 32000237666053 /altid=gi 14764237 /def=ref XP_037763.1 ELK...	875	0.0

Blast hits to dbEST:

CRA Number	gi Number	Score	Expect
CRA 56000140027815	gi 14649878	1604 bits (809)	0.0
CRA 113000033910976	gi 10216507	1463 bits (738)	0.0
CRA 160000136119317	gi 14173010	1417 bits (715)	0.0
CRA 113000033942433	gi 10219367	1417 bits (715)	0.0
CRA 107000020386558	gi 9343047	1255 bits (633)	0.0
CRA 158000041290072	gi 10994272	1223 bits (617)	0.0
CRA 11000545544945	gi 9155653	1187 bits (599)	0.0
CRA 225000001741704	gi 15755809	1158 bits (584)	0.0
CRA 160000136058139	gi 14169810	1152 bits (581)	0.0
CRA 1000491165793	gi 5452865	1130 bits (570)	0.0
CRA 11000545526171	gi 9153925	1059 bits (534)	0.0
CRA 78000106801247	gi 10390259	995 bits (502)	0.0
CRA 147000035349687	gi 12399257	979 bits (494)	0.0
CRA 112000056972111	gi 14374440	979 bits (494)	0.0
CRA 64000081152930	gi 15346261	948 bits (478)	0.0
CRA 11000545400890	gi 9142297	938 bits (473)	0.0
CRA 155000146359590	gi 13327757	922 bits (465)	0.0
CRA 11000545450274	gi 9146937	912 bits (460)	0.0
CRA 45000033524462	gi 8257100	910 bits (459)	0.0
CRA 47000019387182	gi 9775630	908 bits (458)	0.0
CRA 11000545400296	gi 9142242	890 bits (449)	0.0
CRA 118000028616173	gi 10901028	835 bits (421)	0.0
CRA 223000002472058	gi 15688546	690 bits (348)	0.0

FIGURE 1B

EXPRESSION INFORMATION FOR MODULATORY USE:

library source:

gi Number	Organ	Tissue Type
gi 14649878	brain	neuroblastoma
gi 10216507	lung	small cell carcinoma
gi 14173010	muscle	rhabdomyosarcoma
gi 10219367	lung	small cell carcinoma
gi 9343047	lymph	Burkitt lymphoma
gi 10994272	(none)	ovary, tumor tissue
gi 9155653	placenta	choriocarcinoma
gi 15755809	pooled colon/kidney/stomach	
gi 14169810	colon	adenocarcinoma cell line
gi 5452865	colon	colon tumor, RER+
gi 9153925	placenta	choriocarcinoma
gi 10390259	placenta	choriocarcinoma
gi 12399257	placenta_normal	
gi 14374440	colon	
gi 15346261	pooled pancreas/spleen	
gi 9142297	lymph	Burkitt lymphoma
gi 13327757	kidney	renal cell adenocarcinoma
gi 9146937	kidney	renal cell adenocarcinoma
gi 8257100	breast_normal	
gi 9775630	cervix	cervical carcinoma cell line
gi 9142242	lymph	Burkitt lymphoma
gi 10901028	uterus_tumor	
gi 15688546	Pancreas	Purified pancreatic islet

FIGURE 1C

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1  MSSARTPLPT  LNERDTEQPT  LGHLDSPKSS  KSNMIRGRNS  ATSADEQPHI
51 GNYRLLKTIG  KGNFAKVCLA  RHILTGKEVA  VKIIDKTQLN  SSSLQKLFRE
101 VRIMKVLNHP  NIVKLFEVIE  TEKTLYLVE  YASGGEVFDY  LVAHGRMKEK
151 EARAKFRQVV  SAVQYCHQKF  IVHRDLKAEN  LLLDADMNIK  IADFGFSNEF
201 TFGNKLDTEFC  GSPPYAAPEL  FQGKKYDGPE  VDWSLGVIL  YTLVSGSLPF
251 DGQNLKELRE  RVLRGKYRIP  FYMSTDCENL  LKKFLILNPS  KRGTLQIMK
301 DRWMNVGHED  DELKPYVEPL  PDYKDP RTE  LMVSMGYTRE  EIQDSLQVGR
351 YNEVMATYLL  LGYKSSELEG  DTITLKPRPS  ADLTNSSAPS  PSHKVQSVS
401 ANPKQRRFSD  QAGPAIPTSN  SYSKKTQSN  AENKRPEEDR  ESGRKASSTA
451 KVPASPLPGL  ERKKTTPPTS  TNSVLSTSTN  RSRNSPLLER  ASLGQASIQN
501 GKDSTAPQRV  PVASPSAHNI  SSSGGAPDRT  NFPRGVSSRS  TFHAGQLRQV
551 RDQQLPYGV  TPASPSGHSQ  GRRGASGSIF  SKFTSKFVRR  NLNEPESKDR
601 VETLRPHVVG  SGGNDKEKEE  FREAKPRSLR  FTWSMKTTSS  MEPNEMMREI
651 RKVLDANSCQ  SELHEKYMILL  CMHGTPGHED  FVQWEMEVCK  LPRLSLNGVR
701 FKRISGTSMA  FKNIASKIAN  ELKL  (SEQ ID NO:2)

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FEATURES:

Functional domains and key regions:

Prosite results:

PDOC00001 PS00001 ASN_GLYCOSYLATION

N-glycosylation site

Number of matches: 4

1	90-93	NSSS
2	385-388	NSSA
3	480-483	NRSR
4	519-522	NISS

PDOC00004 PS00004 CAMP_PHOSPHO_SITE

cAMP- and cGMP-dependent protein kinase phosphorylation site

Number of matches: 5

1	291-294	KRG
2	406-409	RRFS
3	444-447	RKAS
4	462-465	RKKT
5	702-705	KRIS

PDOC00005 PS00005 PKC_PHOSPHO_SITE

Protein kinase C phosphorylation site

Number of matches: 16

1	3-5	SAR
2	29-31	SSK
3	75-77	TGK
4	121-123	TEK
5	290-292	SKR
6	374-376	TLK
7	392-394	SHK

FIGURE 2A

8	423-425	SKK
9	442-444	SGR
10	449-451	TAK
11	479-481	TNR
12	537-539	SSR
13	584-586	TSK
14	603-605	TLR
15	628-630	SLR
16	634-636	SMK

PDOC00006 PS00006 CK2_PHOSPHO_SITE
Casein kinase II phosphorylation site
Number of matches: 8

1	10-13	TLNE
2	42-45	TSAD
3	75-78	TGKE
4	133-136	SGGE
5	275-278	TDCE
6	338-341	TREE
7	366-369	SELE
8	639-642	SSME

PDOC00008 PS00008 MYRISTYL
N-myristoylation site
Number of matches: 5

1	348-353	GQRYNE
2	559-564	GVTPAS
3	574-579	GASGSI
4	610-615	GSGGND
5	706-711	GTSMAF

PDOC00009 PS00009 AMIDATION
Amidation site
Number of matches: 3

1	222-225	QGKK
2	442-445	SGRK
3	570-573	QGRR

PDOC00100 PS00107 PROTEIN_KINASE_ATP
Protein kinases ATP-binding region signature
59-82 IGKGNFAKVKLARHILTGKEVAVK

PDOC00100 PS00108 PROTEIN_KINASE_ST
Serine/Threonine protein kinases active-site signature
171-183 IVHRDLKAENLLL

Membrane spanning structure and domains:

Helix	Begin	End	Score	Certainty
1	231	251	1.431	Certain

BLAST Alignment to Top Hit:

>CRA|18000005076710 /altid=gil11067437 /def=ref|NP_067731.1|
serine/threonine kinase [Rattus norvegicus] /org=Rattus
norvegicus /taxon=10116 /dataset=nraa /length=722
Length = 722

Score = 1418 bits (3629), Expect = 0.0

Identities = 706/724 (97%), Positives = 715/724 (98%), Gaps = 2/724 (0%)

Frame = +3

Query: 396	MSSARTPLPTLNERDTEQPTLGHLDSPSSKSNMIRGRNSATSAD	EQPHIGNYRL	LKTIG	575
	MSSARTPLPTLNERDTEQPTLGHLDSPSSKSNM+RGRNSATSAD	EQPHIGNYRL	LKTIG	
Sbjct: 1	MSSARTPLPTLNERDTEQPTLGHLDSPSSKSNMLRGRNSATSAD	EQPHIGNYRL	LKTIG	60
Query: 576	KGNFAKVKLARHILTGKEVAVKIIDKTQLNSSLQKLFREVRIMKVLNHPNIVKLFEVIE		749	
	KGNFAKVKLARHILTGKEVAVKIIDKTQLNSSLQKLFREVRIMKVLNHPNIVKLFEVIE			
Sbjct: 61	KGNFAKVKLARHILTGKEVAVKIIDKTQLNSSLQKLFREVRIMKVLNHPNIVKLFEVIE		120	
Query: 750	TEKTLYLMEYASGGGEVFDYLVAHGRMKEKEARAKFRQVSAVQYCHQKFIVHRDLKAEN		929	
	TEKTLYLMEYASGGGEVFDYLVAHGRMKEKEARAKFRQ+VSAVQYCHQKFIVHRDLKAEN			
Sbjct: 121	TEKTLYLMEYASGGGEVFDYLVAHGRMKEKEARAKFRQIVSAVQYCHQKFIVHRDLKAEN		180	
Query: 930	LLLDADMNIKIADFGFSNEFTFGNKLDTCGSPPYAAPELFQGKKYDGPEVDWWSLGVIL		1109	
	LLLDADMNIKIADFGFSNEFTFGNKLDTCGSPPYAAPELFQGKKYDGPEVDWWSLGVIL			
Sbjct: 181	LLLDADMNIKIADFGFSNEFTFGNKLDTCGSPPYAAPELFQGKKYDGPEVDWWSLGVIL		240	
Query: 1110	YTLVSGSLPFDGQNLKELRERVLRGKYRIPFYMSTDCENLLKKFLILNPSKRG	TLEQIMK	1289	
	YTLVSGSLPFDGQNLKELRERVLRGKYRIPFYMSTDCENLLKKFLILNPSKRG	TLEQIMK		
Sbjct: 241	YTLVSGSLPFDGQNLKELRERVLRGKYRIPFYMSTDCENLLKKFLILNPSKRG	TLEQIMK	300	
Query: 1290	DRWMNVGHEDDELKPYVEPLPDYKDPRRTELMVSMGYTREEIQDSLVGQRYNEVMATYLL		1469	
	DRWMNVGHEDDELKPYVEPLPDYKDPRRTELMVSMGYTREEIQDSLVGQRYNEVMATYLL			
Sbjct: 301	DRWMNVGHEDDELKPYVEPLPDYKDPRRTELMVSMGYTREEIQDSLVGQRYNEVMATYLL		360	

FIGURE 2C

Query: 1470 LGYKSSELEGDTITLKPRPSADLTNSSAPSPSHKVQRSVSANPKQRRFSDQAGPAIPTSN 1649
LGYKSSELEGDTITLKPRPSADLTNSSAPSPSHKVQRSVSANPKQRR SDQA PAIPTSN
Sbjct: 361 LGYKSSELEGDTITLKPRPSADLTNSSAPSPSHKVQRSVSANPKQRRSSDQAVPAIPTSN 420

Query: 1650 SYSKKTQSNNAENKRPEEDRESGRKASSTAKVPASPLPGLERKKTTPSTNSVLSTSTN 1829
SYSKKTQSNNAENKRPEE E+GRKASSTAKVPASPLPGL+RKKTTPSTNSVLSTSTN
Sbjct: 421 SYSKKTQSNNAENKRPEE--ETGRKASSTAKVPASPLPGLDRKKTTPSTNSVLSTSTN 478

Query: 1830 RSRNSPLLERASLGQASIQNGKDSTAPQRPVVASPSAHNISSSGGAPDRTNFPRGVSSRS 2009
RSRNSPLL+RASLGQASIQNGKDSTAPQRPVVASPSAHNISSS GAPDRTNFPRGVSSRS
Sbjct: 479 RSRNSPLLDRA SLGQASIQNGKDSTAPQRPVVASPSAHNISSSGAPDRTNFPRGVSSRS 538

Query: 2010 TFHAGQLRQVRDQQNLPGVTPASPSGHSQGRRGASGSIFSFTSKFVRRNLNEPESKDR 2189
TFHAGQLRQVRDQQNLP+GVTPASPSGHSQGRRGASGSIFSFTSKFVRRNLNEPESKDR
Sbjct: 539 TFHAGQLRQVRDQQNLPGVTPASPSGHSQGRRGASGSIFSFTSKFVRRNLNEPESKDR 598

Query: 2190 VETLRPHVVGSGGNDKEKEEFREAKPRSLRFTWSMKTSSMEPNEMMREIRKVLDANSCQ 2369
VETLRPHVVG GG DKEKEEFREAKPRSLRFTWSMKTSSMEPNEMMREIRKVLDANSCQ
Sbjct: 599 VETLRPHVVGSGGTDKEKEEFREAKPRSLRFTWSMKTSSMEPNEMMREIRKVLDANSCQ 658

Query: 2370 SELHEKYMLLCMHGTPGHEDFVQWEMEVCKLPRLSLNGVRFKRISGTSMFAKNIASKIAN 2549
SELHE+YMLLC+HGTPGHE+FVQWEMEVCKLPRLSLNGVRFKRISGTSMFAKNIASKIAN
Sbjct: 659 SELHERYMLLCVHGTPGHENFVQWEMEVCKLPRLSLNGVRFKRISGTSMFAKNIASKIAN 718

Query: 2550 ELKL 2561
ELKL
Sbjct: 719 ELKL 722 (SEQ ID NO:4)

Hmmer search results (Pfam):

Scores for sequence family classification (score includes all domains):

Model	Description	Score	E-value	N
PF00069	Eukaryotic protein kinase domain	346.8	2.3e-100	1
CE00022	CE00022 MAGUK_subfamily_d	59.5	1.8e-17	3
CE00359	E00359 bone_morphogenetic_protein_receptor	19.6	7.5e-05	2
CE00334	E00334 urotrophin_receptor	12.7	0.00057	2
PF00627	UBA domain	12.5	0.096	1
CE00031	CE00031 VEGFR	4.0	0.25	1
CE00203	CE00203 ERBB_RECEPTOR	3.0	1.7	1
CE00287	CE00287 PTK_Eph_orphan_receptor	-16.2	3.4e-07	1
CE00292	CE00292 PTK_membrane_span	-21.5	6.9e-08	1
CE00291	CE00291 PTK_fgf_receptor	-35.7	1.2e-06	1
CE00290	CE00290 PTK_Trk_family	-65.9	5.2e-11	1
CE00289	CE00289 PTK_PDGF_receptor	-68.0	0.4	1
CE00286	E00286 PTK_EGF_receptor	-75.9	1.8e-06	1
CE00016	CE00016 GSK_glycogen_synthase_kinase	-179.5	1e-06	1

FIGURE 2D

CE00288 CE00288 PTK_Insulin_receptor -208.8 0.01 1

Parsed for domains:

Model	Domain	seq-f	seq-t	hmm-f	hmm-t	score	E-value
CE00022	1/3	59	131 ..	23	98 ..	10.3	0.0061
CE00359	1/2	54	141 ..	142	233 ..	5.7	0.64
CE00289	1/1	52	155 ..	1	109 []	-68.0	0.4
CE00022	2/3	157	183 ..	128	154 ..	14.5	0.00034
CE00031	1/1	172	195 ..	1068	1091 ..	4.0	0.25
CE00203	1/1	171	195 ..	861	885 ..	3.0	1.7
CE00334	1/2	172	197 ..	678	703 ..	11.1	0.0018
CE00359	2/2	171	201 ..	272	302 ..	14.5	0.002
CE00334	2/2	230	240 ..	738	748 ..	-0.3	7
CE00288	1/1	55	281 ..	1	269 []	-208.8	0.01
CE00022	3/3	211	292 ..	188	271 ..	34.3	4.9e-10
CE00290	1/1	54	302 ..	1	282 []	-65.9	5.2e-11
CE00291	1/1	53	302 ..	1	285 []	-35.7	1.2e-06
CE00286	1/1	53	302 ..	1	263 []	-75.9	1.8e-06
CE00292	1/1	53	302 ..	1	288 []	-21.5	6.9e-08
CE00287	1/1	53	302 ..	1	260 []	-16.2	3.4e-07
PF00069	1/1	53	304 ..	1	278 []	346.8	2.3e-100
PF00627	1/1	332	362 ..	9	41 .]	12.5	0.096
CE00016	1/1	2	412 ..	1	433 []	-179.5	1e-06

FIGURE 2E


```

1 TCTAGGCGGG GAGACAAGCT CAGCAGCCTT GTGCAAAGCT AGCAAGGAAG
51 AGAAAGGATA GGTAGGGTAG GGGTTGGGGA TGAAGGTCAA AGGGCAGGGG
101 TGAGGCAGGG GTTAGAGCTA GAGTGAGAAG CTTGGAGAAG ATGGAGTCTA
151 TTTAGACGAG AGTGTGGACC AGGGAGAGAC TGCTGGAACA CCAACCACCA
201 ACTGCTTCCT CTCTCTTTTC CCTGCTTTCC AGACCCTGGC ATTAGAGGTG
251 ATACCAGGCA CAGGAATCAG CAACGTGTCT CCCTTTGGCC ACCAGAGGGC
301 AGATGATTCT CAAGGATCGA ATTTGGGTTG GGGAGTGAGG TGTTCTCTGT
351 CCTCCTCTTC TCTCTTTCCC TCACCTTCAT GGGTGTGCCT TCACCTTCTT
401 CCTCAACGGT TGGGTGCCTG AATAGAGCTG GTATGGGGCA TGGGGAGCAG
451 TGCTGAAGTC CCAGGATTTA CTAAGAGTGT AGTGATACCT GTTGCCTTAG
501 GAAGTACTTT CATAACCTGG TAATTACATC TGCTCAGATG CCTATTTCTC
551 TGATTGATGG GATGAAGGCT GGCTCAAGAT GCTGTAGCTG GGAGTTGGAG
601 GTCAAGTAGC AGGGGTCCAA TCAGCAGTTT TCCCAATAAC TCCTGGAGCC
651 TCTCTGCTCC TGTACCTTTG GGAACCTGTT GCCTGAGTCT GGTTTCTGAC
701 TCCTGCGGGG CCTCTGCCTC CTGCCACCT TAAGCCACTG ATGGGAGGGT
751 GTGGTTCCAA CGTGTTCAG GTACTATGGG TGAGGACAGC TTGGCGCTGG
801 GGAAATCAGC CCAGGATACT CCCTGTCCTT GGTAACGCAG TGTAAGGGGA
851 AGTGAGGAAT GGACTGCACT TGCCATACAG ACTTCCTGTT AGTCAAGGGC
901 TCTCCAAAGC TGAGAAGGAC CTCCGAGTTC ATGAATCCAA TGGCTTCACT
951 TTA CTGATGG GGA AAATGAG GCCCAGAGGA GGAAAGAAAA GAAACTTTAA
1001 ATGCCTTATC TTGCAGAGGC ATTTTAAAAG GTA ACTGGAA TTCAGAAATG
1051 TCATTTTGAA TGTCAACGCA GGAGCAAAGG CAAAGGAAAG AGGAGCCTAA
1101 ACTCAGTGAT GTTATGTGAT TTTTCCAAGA TCACGCAGCA TTGGCACTTG
1151 GCAGAGCTGG GGCTGAAATG CAGGGCCCTG GACGCTCCCG CATCCGGTGC
1201 AGAGGACGCT GCCCTGGGCC TGCCTGGGGC CTTGCCGAGC CCTGCGGACT
1251 AGATGCGGGA ATGCACGGAT GAATCCACAG AAGCCAAGAT AGACGGTGCC
1301 AGACAGGCAA TAGACTGATG CTGCATTGTA CAGGTATATT GATAGGCTAG
1351 ATGATAAAAA GAAGATGAAT TTTATGAGCT GACCGACAGA TGGACAGAAA
1401 TGCAGACAGG AAGCTGCTAT AGAACCAGAG GATGCCAATC ACAGGGACGG
1451 CTAACAATCT TGT TTTGTAT TTAGTCAAAT CACAAGCACA GACAGGTGAC
1501 CCACGCTTCC TGT TCAAGT TGA AAATGC CCG AAAACTG ACGGAAAGAC
1551 ACGAAGCGAA TCAGACTCCG AGAGCCACCC GGGGAAACGA CCGGGTGCTC
1601 GGAGGGCCTC GGGTGT TGCC GGA AATGGCC GACGACCGCC CTCGGCAGGG
1651 CTGTGGGAGG GGGCGTGGCC GGCTCAGCAC GCGGAGCAGC TTCGGGTATT
1701 TCCGGAAACT GCCGAAAGCC CCCTTGAAGT GGGCGGGGAA AGGCCGGTGG
1751 GCGTGGCTGG ATGGCCGTGG ACGGGGGCGG GGGGTAGGCA CCCGGGGTCG
1801 CTTCTGTGAT TTCCGTAAAC AGAGCCGAAG CTTCTGTCTC GGAATCGAGG
1851 AGGAGAGCGC GTCCCCGGGG TTTACCTTCT TCGGCTGTTT CCGGAATTCA
1901 CCCGTAGTCT GTGGCCGGGA GGAGAAGGCG CGCCCCACCT CCCGTTTCTA
1951 GCCGCTTCGG ATGTTTCCGG CTGCTGCCGG CGAAAAGAGC CGAGGGCCGG
2001 CGGTGGTGGC GGCCATGTTG GGAGCAGCAG GTCCGGCGGC GGCTGCCTGT
2051 GTGCCGGGCG CGGAGCAGTG CCGCTGAGGG CAGGGGAGGA GCGAGGCAGG
2101 CGGCCGGCTG CGGCGGCAGA GAGTAGGCGG AGCGGCGCGG CCCGGCCGAA
2151 AGGCGGCACA GCCCAGCCGG GGGTCGGGGG GGTGCGGTCC GGAGCCGCTC
2201 GGAGCCGGCG CGGCCTAGCC CGAGCGGCGC ATCCCCGGGC TGGCGTGAGC
2251 GGCTGCCCGG CCTCCCCGCA CCCCCGGCCG GGGCCCATGC GGCGGGTGCT

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FIGURE 3A-1

2301 CCTGCTGTGA GAAGCCCCGC CCGGCCGGGC TCCGCGCCTT CCCTTCCCTC
2351 CCTTCCTCCA AGCTTCTCGG TTCCCTCCCC CGAGATACCG GCGCCATGTC
2401 CAGCGCTCGG ACCCCCCTAC CCACGCTGAA CGAGAGGGAC ACGGAGCAGG
2451 TAAGGAGCCC CGAGGGCTCC CCGAATTCTC TGGCTGGGCC CTTTGCACCT
2501 TGCGGAGCCT CCTCCCTCTT CTGCTCTCCT CGTGCCCCCTG CTGCCATCCT
2551 GCAAGCCTCG GCTGCCCTGT CATCCGGCTC CTGGCTCCGG CTCCGCACAT
2601 CCCGCTTCCG AGTCCTGACC TGGGACCCAC CTCGTCCTGA CTCCAAGCTG
2651 CACACTTGTC TTTCTGCCAA CCCCCGTCTC CCCTCACCGC CCTCCTGCGC
2701 TCTTCCGTGT CACCTCCCCA GCTTCCCTTT CTCTTCCCTT TTTCTCTCAG
2751 GGGCCTTTCT GGTCTTCTCT CACCCACGCT TAAAGCAGCC ACCCTCCCCG
2801 TCCTCGAATA GCAGCACCCC GCGATTTGCC ACAGATCGTT GTCCACCTCT
2851 CCCTTCGTCT CTCCTGCCTC GCTTCCCCTC CGCCCGCACC GGTTCGCGCA
2901 GTCTCTGGGT TATCACCTC AGGGTCCTTG CCCTGGACTG CGCTCTCGAT
2951 CCCTGGCCCC TTGCAGTTCC CCCAGCTTTT TCTACCCTGC TTCTTCGTTT
3001 TCCAAATTGT GCTCTCCCTC TTGCTTGCAA CCCACCAGCT CCACCCTCAT
3051 CACCTTTCCA AATCCTTCGC CTACTCTTTG CTCATCACTT TCCCTTCTTT
3101 GCTCCAGGAG CTCCCTGGAT CCTGGCGCTG GCATTTGTCTG CTTCCGTGTT
3151 TCCCCACAGC TGTATGCGC ATAGTTTTCC CACAGGTTGC GTTTGGGGTT
3201 CCAATCATCA CTCCTTCAG AGTCTTTGGA TCCCTCTGT TCTCTTCCCC
3251 TCGGGTTTGG CTTTTAGGTC CCTGGGCCTC TTGTTTCTCT CTGTGAGTGT
3301 TCTACCAGCC TTCTACTGGG CTCTTTCTCC CAACCCAAAG ACACTTGGCC
3351 CCACCGTATT AACACAACCT GTTGCTCAGT CCTTTCCCAG ACCTCGCTGC
3401 ATCACAGTTT TTGCCTTTCT GTCTTCGTAC GCTGGAACAC AAACCATGAT
3451 GACTTTCTGT GTCTTCACTC CCGTGCCTGG CACTTAGAGT ATTTTCTTTC
3501 TTGCTTGTTG CCTTCCTGTT TCTCCACCCT CACCCCATCT TCCTTACTGT
3551 GCCTTTTAAT CAGCGTTGCC TTTTATCTCC GCATTAGTCT CCTGCCTTCT
3601 TCATGTCCTG TGTATCCCCA CACCGTGCTT GGATCCATTC TGTTCTTATT
3651 GGCTAAGTCT CTGTAATGCC CAGGAAGTCC AGGTGTTTTG CATGCTAGTT
3701 TCTTGAGCTA CACCTCAGCC TCACGACTCT ACACGGTCCC CCTCATCCTG
3751 GCAGTCACTG CTATGTTTTT CACCCAAGTC TTAGCCTTTC TGTGTCATCT
3801 CACTTTTGAT CCCAGAGACG TCCACTTTCC ACACCTCCCC TTTATTTTCA
3851 CATCTCTAGC GTCCTTTGCT GACTGCTCTG TGCAGAGTCC CCTGCCTGTC
3901 ATACCTTTCT TGGTGGAGAA CTTTACTAGG CCAAAAAAAC TTGACTTGAA
3951 AAAGAAGTGC TTCTGCCCCG GGGCTGCTGT GCTTTTTGCC TTCTTTCCCC
4001 TCCTTCCATC CTTTATGTTT CCCTCTTACT CCCTTCTTTC TTTGTAGCCC
4051 GGTAGAGCAG TTGTTGTATT CTCTTGCATG TGAACATTCT TCTTTGAAAA
4101 ATCTTACCTC CTTTCTTTTA CTGTGTTTTT CTATTTTGTT ACCCCCTGGC
4151 CCTCTGTCAC CTGGGCAGTT AGGAACTAAA GAGAAGTTCT AGGCAGAGTT
4201 TTTCTCTGCA GGGTTGACCC TTTTATTACT TGTGGATTAT TTGCTTCTGG
4251 GGGTGAAATA GGGGTTGAGA GGGAGGGATG GTTGATTTC ATTTTCATCAC
4301 TGGGTTTGGC AGCTGGTTCT GCATGGGACA GGGGTCCTTG GAGACAGAGG
4351 AGCATGTTCT GTGTCTCGCA GTCTTTCTCT CCCTTGCCTA CCGGCTGTTT
4401 CTCTCTCCTT ACTGGGAATT GCTTTCTCTG GGCCCTCTTG AGGTTGCTTA
4451 TTCCACCCAT TTTCCTCTCA CAACCTTTGT TTAGCAGGT AAACCCTGCT
4501 TAACCAGAGA ACTTTCCCAG ACTGTTGATC GTGAGCTGGT AGGAGGAGGC
4551 CAAGTGACTG ACTGGCACCC TCAGGCATTT GGGGAGTGCC GATGGAGTGC

FIGURE 3A-2

4601 CTA CTCTCAG TGAGGCTGGT GGGGGGCATT GTGTTCAGCA GAGCAGAGTA
4651 ACAGACTGCC TCAGTGTGGT TTCTTTGTGC TGCTTACTAC ATGTAAATGT
4701 ATTATTGCCA TGGTATTTTT CCTGTGATGT GTGTGTTGAT TTCCTTTCTT
4751 CCTTACATGC CTAGCATACT GCTGAGCATA TAGTAGGAAT TCCACCGTAG
4801 TGTGCATCCA CTGATTCCAT GATAGCAGCA ATCAGTGACC ATTTGGGAAT
4851 GTAAGTAAGC TCTTTGCTCT TTGATAACTT TGCCCAGAGC AGTAGCTGCA
4901 TACATTGTCA TCCTGTTAGG ATTATTAATT ACCCATCCTA TTTCTACTCT
4951 TTATGGACTT AGATTCTCCT TAGCCCCTTC ATACCTTCTA CTGTTGTTCT
5001 CAGGGTAGCC AGTCACTGTA TCGATTTAAT ATTAAGTCTC ATTCCAGTAA
5051 AAGCAGGGAC TTTGGAAAAC CTTGGATGCA CCTATTCCAG ACAGATTCTT
5101 GTATTCTTTT TTTTTTTTTT TTTTGAGATA GAGTCTCGTT CTGTCGCCAG
5151 GCTGGAGTGC AGTGGCACAA TCTTGGCTCA CTGCAATCTC CGCCTCCTGG
5201 GTTCAAGCGA TTCCCTGCC TCAGCCTCCT GAGTAGCTGG GACTACAGGC
5251 ACACACCGCC ACGCCCGGCT AATTTTTTGG ATTTTAGTAG AGACAGCGTT
5301 TCACCATGTT GTCCAGGATG GTCTCAGTCT CCTGTCCTCG TGATCCGGCC
5351 TCCCAAAGTG CTGGGATTAC AGGTGTGAGC CACTGCGCCG GGCCTGATTC
5401 CTGTATTCTT TAAAACGGGA AAAAAGACAA GCAGCAGCTC CTCAGGTCAC
5451 AAGGCCAGGT ATATCAACA CTGGCCTCCG AGAATAGATC ATGCCACCAA
5501 GTGAAAGAAA CCTCTTCTTG GTCCTGTTGT GATTTTAGAT AAAGTAGTCA
5551 TGGAAGCTTG GTCATTACTA TAGTCTTAAT GTTATTTTTT TAAAAAGGG
5601 GATTTAGTTG GGCTGATTTC CTCCCCTAAA GGTCTCTGT CACCTTATTT
5651 AAATTTAAAA CTGGTTTTAC CAGAAAATAG GTAAACAAAC ACCACTGGTT
5701 GTCTCCAGTC TCTTTTCTTG CTCTTCCTCT CCCTCTTCTT TAAAAATGTG
5751 GCTGATGAGA ACCTGTTTCC AGGAGCCCTT TAATCACTCT GAAACACACA
5801 GACACTGAAA ATGTTGAAGC ATAAAAATAA ACCTTGCGTT ACAGGGAGAT
5851 TGCCTGTGTG CTGTCCACTT CGCTTATAAC AGTGAAAGTA GGAGATTAAA
5901 AAAAAAAAAA AGTTAAGCCC TGTCTTTAAG ATGGTTTTTG TGACACCTGA
5951 TTCCAGATGT GCTTTTTTAC AGCCATAGAC TTCCTGCTTT TGCAGAAGGA
6001 GGGTTCTAAT CTGGGGCTCG TAGCTTGGGG GATTCTTAGT TTGTGAGCTG
6051 AGCTTTTTGT TCACTTCTTT TCCAAATGAC TCTGCTGGCC TGAAGCTTGG
6101 CAGTTGTGAA AGCAATCAGC AAGATGACTG TTTGTCTTCC AGCCAGCAGC
6151 AGCAGTCACA GGCAAGCCTG GAGAAAGGTC CAGCTTCCAG AGTTCACCTG
6201 CTAGAGTTTT CCATAACACC TGGGGGAGAG GCTACTCCAT CTGGGACCTG
6251 CCCCACCTCT GGGCCTCAGA AACTATGAGA GAGGGATTGA GAGAAAACCT
6301 GCCCCACTTC TGCTGCAGTG GGAAGGGAGG GGGCTGCTGT CAGGCTTCTA
6351 GGCAGTGAGC GGCATTGTTT ATTCTCTCAG TTCTAGGAAG GGGAGTTTAG
6401 AAGTACTGGT GAAGAAAACA AAGTTACAAG ATCCTATAAG GAACAGCTGA
6451 ACTACTCCAA ACACTCTCAC TGGACCCCCA TTGTTGATTC TGGATAAAAA
6501 TATATATATA TATAAACTC TTTTTTTTTT TGACACAGAG TCTTGCTCTG
6551 TCGCCCAGGC TGGAGTGTAG CGATGCGATC TCGGCTCACT GCAACCTCCG
6601 CCTCCCGGGT CAAGCGATTG TCCTGCCTCA GCCTCCTGGG AGTAGCTGGG
6651 ACTACAGGCG CCCACCACCA TGCTGGCTAA TTTTGTATT TTTAGTAGAG
6701 ACGGGGTTTT GCCATATTGG CCAAGCTGGT CTCGATCTCC TGACCTCAGG
6751 TGATCTGCTG GATAAATATT TTTTTTTTGC TTTTGGTGTA ACTTAGGTAG
6801 ATTGATCGG CTAGCTAGCA TCTCAGTCCA CACTCTGAGC TGTGCAGCAG
6851 TGTGCCCTGG TGCTAATTCT CACTCTGTCC TTTGATTCTG GCCAGGGGGT

FIGURE 3A-3

6901 CCTTGGTGGT GCTGCCTTCT GGTGAGGAAT GTGGGTGAAT GTCAGACCAA
6951 ATAGTGTAC TTTGGGCTTG GCCCTAGAGA TCAGGAAGGA AGTGTGTGTA
7001 GAGCAAGGGC TTTGGGAGTC CTTGGAGTTC GTAACCTTTG AATCTGAAAA
7051 GTAACGTAC CTAGTAAATT AGAATAATTT CTCTCTGGTC AGGCACCATG
7101 GCTCATGCCT GTAGTCCTAG CACTTTGGGA AGCCAAGGCA GGAGGATTGC
7151 TTGAGGCCAG GAGTTCAAGA CCAGCCTGAT CAATAAAGTG AGACTCCATC
7201 TCTACAAAAA AATTTTTTTA AATTTAGCTG GGCATGGTGG CACATGCCTG
7251 TGGTTGCAGC TACACAGAAG GCTGAGGCAG GAGGATGGCT TGAGCTGGGG
7301 AGGTCGAGAC TGCATTGAGC TGTGTTTGTG CCACTGCACT TCAGCCTGGG
7351 TGACAGAGCA AGACACTATC TCAGAAAAAA AAAATTACTT TTCTCCAATT
7401 TATGGACTTC GGAAAGTAGC TAAACAGATG GATATAAGAC AGTTGTTGAA
7451 ACTCGGCCTG CTGCAGATTA AAATAAAGTT TGCACAAGGA TAACTTAATC
7501 TTTGAGACCA ACCAAAGTTT GGGCTGGAGA TTTTCTCAG CATAAATGTC
7551 CTAAGCAGAG TTGGTGCCTA TGAGGTAGGA AAAGATTGAG ACTTTGCTTG
7601 CCTAAGAGGT TTGCAGGGT CGAGCTTTTG GGAGTCAGAA CTTCTCAGAC
7651 TAGATTGTTT CCCCTTTGGA CAGAACAACC CAATTCTCAG TGGGCATTTG
7701 ATCAGGACTA ACCCAGGCCT TCATGAACTC TTTCCCATTG AGCACTTAGC
7751 CACCTGGCTG GCATTTCTCT TCTCCAGGA GCTTCCATGA GGTTCCTACT
7801 TATGTATTAT GTCGACTTGA ATGAATATTT TATGTCTAGA GTGCAGCCAA
7851 GCCTCAGACT TTGTGGCCCA TTATCGACAA ATGGGGTAGG GGGTGGGCGC
7901 CACCTTTGGC CCCGTGATAG CTTCTCTGCT AAATGGACTC CCCCAGCAG
7951 CACTTTGAAG CCCATTAATG GATTGGAATG AAGTAACCTC AGCAGATGGA
8001 AAGGGTGAGG AGGGTGGTCA TCTTCCTTCC CTGAGACTGC CTGATGAGGC
8051 TTTCTACAG TAACCAGGAC AAGCCCCTAT TCCCTCTGCT TGGTTAAGCT
8101 GTGGACTGGA GCTACTAGGC CTCTGCTTTG AGAGGAAGTA TAGAAAGGAT
8151 TTGATTCTCT TTTAGCCATG GTGGGGCCGC CAGTTTCCCC ACTTTCCCAT
8201 CAAAGCAAAA ATTGAGAAGG ATGTGGAAAG GGTGGGTGGA GTTTAAAGCT
8251 GGCCCTTCCT CCTTCAGTGG AAGTTCAGCA AAATGACAAA CCAGATAGGT
8301 GGCTAAATTT CTTCTCTTG ATGGGAGATT CCAGTATTTG TACGTTTTGT
8351 GCTTGTAGCT TGGATTCTCC AGGCCTCCTC CCAGCTTTCA TCAAACATGA
8401 GTGAGTCACT GAAGTGTGT CTATGCATTT TCTCCCTTCT GTCTCTGCAA
8451 AGGGAAGAGT AAGCCTTTAC AAACCTGTGG GGGAGGAAGT CACCCTCTTC
8501 CCACTGCTGG AGAGCCAGGC TATCCCCAGG TTAACCCTGA AAGTGCTAAC
8551 TCCTGAGCAG AATGTTACTG CCACCCGCCC CTTCTCTTTT TGTATAGGC
8601 CATTGAAGGT CATTGCTCGT CTTTTTTTTT GAGACAGTCT TGCTCTGGTC
8651 ACCCAGGCTG GAGTGCAGTG GCAGGATCTC AGCTCACTGC AACCTCCACC
8701 TACTGGGTTC AAGCGATTCT CATGCCTCAG TCTTCCAAAT AACCAGGATT
8751 ACAGGTGCGC ACCTCCATGC CTGGCCACTT TTTGTATTTT TAGTAGAGAT
8801 AGGGTTTCAC CATGTTGGCC AGGCTGGTCT TGAACCTCTG GACTCAAGTG
8851 ATCCGCCTGC CGTGGCCTCT CAAAGTACTG GGATTACAGG AGTGAGCCAC
8901 CGCGCCCGGC ATCATTGCTT ATCTTTTAGA CTGAGATAGT ACAGCTGATT
8951 CTAAACAGCA CCCAGAGAGA ATCTGGCCTC TTGATTTCCT GTTGTGTCTC
9001 AGAGGAGGAG GCATCCAGT TCCTCCTCTT GCCCTCTAGA CATCTCCTCC
9051 TCTGATAAGT ATAAATAGGC TAGATCCCTT TATCTTCATA TCTGTTTTTG
9101 TCTGGAATGT TTCAAGTTTC TCAAGCTAGG TGTGGTGGCT CATATCTGTA
9151 ATCCCAGCAC TTCGGGAGGC CACGGCAGGA GGATCACTTG AGCCCAGGAG

FIGURE 3A-4

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9201 TTCAAGACCA GCCTGAGCAA CATAGTGAGA CCTCATTTCT ACAAAAAAAAA
9251 AATTTTTTTTT TTGAGACAGT CTTGCTCTGG TCACCCAGGC TGGAGTGCAG
9301 TGGCAGGATC TCAGCTCACT GCAACCTCCA CTTACTGGGT TCAAGCGATT
9351 CTCATGCCTC AGTCTCCCAA ATAGCTGAGA TTACAGGTGT ACGCCACTAT
9401 GCCTGGCTAA TTTTGTATT TTTAGTAGAG ATGGGGTTTC ACCATGTTGG
9451 TCAGGCTGGC CTTGAACTCA TGACCTCGTG ATCTGCCTCA GCCTCCCAAA
9501 GTGCTAGGAT TATAGGCATG AGTCACCCCG CCTGGCCAAA AAAAATTTTT
9551 TTTTTTTTTT TGAGACGTTG TCTTGCCCTG TCGCCAGGC TGGAGTGCAG
9601 TGGCACGATC TCGGCTCACT GCAAGGTCCG CCTCCCGGAT TCACGCCATT
9651 CTCCTGCCTC AGCCTCCCGA GTAGCTGGGA CTACAGGTGC CCGCCACCAC
9701 ACCCGGCTAA TTTTTTGTG TTTTCAGTAG AGACGGGGTT TCACCTTGTT
9751 AGCCAGGATG GTCTCGATCT TCTGACCTCG TGATCCACCC ACCTCGGCCT
9801 CCCAAAGTGC TGGGATTACA GCGGGGAGCC ACCGCGCCCA GCCCAAAAAA
9851 ATTTTTAAAA AGTTACCTGG GTGTGGTAGC ACATGCGTGT ATCCCACCTA
9901 CTCAGAAGGC TGAGATGTGA GGATCACTTG AGCCTGGGAA GTTGAGGCTG
9951 CAGTGAGCTG TGATCATGCC ACTGCATTCC AGCCTGGGCA ACAGAGTGAG
10001 ACCCATCTC AAGATAAATA AGGTTTGTCA GTCCCTGTGG TGGTCTTTTC
10051 CGCAGATGTC TGTCTTTGGG TTGGCACTTA TTCCCCCTA CTTCAGTTA
10101 TTCCTTACAT TTCTCATTAG AAAATGGCAA AAAGGGCAAA AGTAAATTCA
10151 TTTCTTTTTT ACACCAAATC ATTAATTTTA GGCTTATAAA ACTAAATGAA
10201 CAGAAGATTT GGTAGGAGAG GAGGGGAGAT GGACACTGAT ACTGGTGGCT
10251 AGGTGATCCT GAGGGACAAC TGGTGCCTGG CAGAAAGAGA GGAGGGCTGT
10301 GTTCAGTGAC TGGCTCCCAG CCACCTTTTT GGCCTTTTTC TTTTAAACAT
10351 GAGGAAGGCG GAGCAGACCA GGGGCTTCTC TGTAGAACCA GTCAAGCTGG
10401 TTTTGGGCAG CCTTGGCCTA TTTCTTTGTG TGCTCTTTGG GAAGTTGGCA
10451 ATACAAAGGT CTGCCTCCTT TGGGGCTGTG TTCGTTGAGG CGAAAGTTTG
10501 GAAGACAACCT ATCTGTCAAC AACCCCTTTC TCCCAAAACA CTGAATGGGT
10551 CTCTGAGCTG GTCCTTCACT CCAGGGAGGA GGCTTTCTCT CCACCCTATG
10601 CTGAACCTGA AGGCAGCTTT GCTTTATACA CTTTCACTG AAAGCTCTAA
10651 GACATTAACCT CCTTTTTTGG ACTCCCTTCC CAATTCACAA CTTGGTGAAG
10701 GACCCTCAGC CTAGCCAGGA GGAAGGGACT GGGTCTGCCT TTGGCTCCTC
10751 ATTTATGGGT CTGGGAGGGG ATCAGGACTC CTTACTGCTA TGATCTGGCT
10801 GCTAAATTCA GTGACATCCC AGGCCTTTTT TCGTCCACGC AATGGGACTG
10851 TCTGTCCAGG CCTGCTGGGA AAGAAAAGAG AGAAAAAATA GTTTTTGCTC
10901 TTTGGCAGCT TACAGGGACT TCAGCCATAG GAAACAACCT GTAGGAAAGG
10951 TGGGAGCTTC CGGTCACCAT GTGTGCTGAC ACTTCTGCA ATAGCACTAG
11001 GGAGTCTTTC TCAGGGAGCA AGGCCAGCCA GGTAGGATTA TTTCCAGTC
11051 TCCCAGCTAA GCAGGAAATG CCAAATATG AACGTTTAGT AATTAGTGAG
11101 TGTAACCTACC TGCTGACAGA GCTCCAGCCT AGACCTTGTC CTTGGGGGCT
11151 GGTTGCCCCCT GTTGATACTA CAGTGAGCTA CTCATTGCTT CTGATTACCA
11201 TTTCAGTATG AGTTTTGCTT TGGTTTCTGA TATCCCATGT GCGGCTGCCT
11251 TTTTCTCCA CTTCTTTTTT GTTGTGCTT TTTGTTTTTT TGAGACGGAG
11301 TCTTGCTCTG TTGCCAGGC TGGAGTACAG TGGCACAATC TCAGCTCACT
11351 GCAACCTCCG CTTCCAGGT TCAAGCAATT CTGCCTTAGC CTCCCAAGTA
11401 GCTGGTACTA CAGGCATGTG CCAGCACACC CGGCTAATTT TTTTTTTTTT
11451 TTTTTTGAGA CAGGGTCTCG CTCTGTCGCC CAGGCTGGAG TGCAGTGGCG

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FIGURE 3A-5

11501 CGATCTCAGC TCACTGCAAG CTCTGCCTCC CGGGTTCACA CCATTCTCCT
 11551 GCCTCAGCCT CCCGAGTAGC TGGGACTTCA GGCGCCCACC ACCATGCCCCA
 11601 GCTAATTTTT TGTACTTTTT TTTTTTTTAA AGTAGAGATG AGGTTTCACC
 11651 ATGTTAGCCA GGATGGTCTC AATCTCCTGA CCTCATGATC CACCCACCTC
 11701 GGCCTCCCAA AGTGCTGGGA TTACAGGCGT GAGCCACCGT GCCCCGGCTGT
 11751 AACACCTGGC TAATTTTTGT ATTTTATAGTA GAGATGGGAT TTCACCATGT
 11801 TGGCCAGGAT GGTCTCGATC TCCTGACCTC GTGATCCGCC CGCCTCGGCT
 11851 TCCCAAAGTG CTGAGATTGC AGGCGTGAGC CACCGCGCCT GACCTTGTGT
 11901 GTGTTTTTAA GAGACAGGGT CTCACCCTGT CACCCAGGCT AGTATGCAGT
 11951 GGTGTGATCA TAGCCCACTG CGGCCTCAA TAGCTCCTAG GCTCAAGTGA
 12001 TTCTCCCACC TTAGCTTCCA GAGTACTGGG ACTACAGGTC ACACCTGGCC
 12051 CCCTCAACCT TCTGGACTTT TCACTACCC CATCACTCCC TACTTCTCCG
 12101 CCACAGAAGA CTGTCATTGG CTATCTTTGC AAGTAGTATT GAAGCCACTC
 12151 GGAGATTGTT GCTTTGTCTT TTTGCTCATG AAAGTTTGAA TTAAGAGTTC
 12201 TCCAGTCACA GGAAGTGGGG CTCCTTAGGC CAGCTCCATC TCACGTAGTG
 12251 TACTGATTAT GTTGAGCTTA TGGCACAGCT GAGAGGAGAG TCCAAACTTT
 12301 TTGAACACTT TTTGACTTCC AATAAGTGGT TCCACTATGG TTAAGAGCAG
 12351 GTTTGGTGGG CCGGGCGCGG TGGCTCATGC CTGTAATCCC AGCACTTTGG
 12401 GAGGCCAAGG CAGGCGGATC ACCTGAGGTC AGGAGTTCGA GACCAGCCTG
 12451 ACCAACATGG TAAAACCTTA TCTCAACTGG AAATACAAAA ATTAGCCCCG
 12501 TGTGGTGTTG TACACCTATA GTCCCAGCTA CTCGGAAGGC TGAGGCACAA
 12551 GAATCACTTG AATCTGGGAG GTGGAGGTTG CAGTGAACAG AGATCATGCC
 12601 ACTGCACTCC AGCCTGGGCA ACAAAGCAAG ACTTTGTCTC AAACAAACAA
 12651 TAAGAGCAGG TTTTGCGGCT AGATTTCTTG TATTGGAATC CTGGATCATC
 12701 CTCTCCTGTG ATCTTAGGTT CCCTCTGTGT CTGTTTGCTC ATCTGTAAAA
 12751 TGGGAGAAGA ATAGTACCCA TCTTATAGGT ATAGCTGTTA TGAGTATTAA
 12801 AAGAGTTAAT GAATAGAAAG CATTTAGAAT AGCGCCTGGC ACAGCAGAAT
 12851 GATCATTGTC ATTATTGTTC CAGTTGAACA ACACAGTGAA TTTTATCTGA
 12901 GCACCACACA ACTCTAGGTC AGTATAAGGG GTGATGTTTG GGATTTCTCT
 12951 GTAATCAGTT GAAAAAATCT TGTTCTGGCA TCTTCAAGCC ACTGGGGTCC
 13001 TATAGGTGCT TTTTCTAACA TTTCTGTTTT TTTGTTTGTT TGTTTGTTTT
 13051 TTTGAGATGG AGTCTTGCTC TTGTTACCCA GGCTGGAGTG CAGTAGCACC
 13101 ATCTTGGCTC ACTGTGACCT CCACCTCCA GGTTCAGCG ATTCTCCTGC
 13151 CTCAGCCTCC CAAGTAGCTG GGATTACAGG CACCTGCCAC CATACCTGGC
 13201 TAATTTTTTT TTTTTTTTTT TTTTTTTTTG TATTTTTAGT AGAGATGGGG
 13251 TTTACCATG TTGACCAGGC TGGTCTTGAA CTCCTGACCT CATGATCTGC
 13301 CCACCTCGGC CTCCCAAAGT GCTGGGATTA CAGGCGTGAG CCACTGCACC
 13351 CGCCCTAGTT TGCTTTTTTA CCAATCACCT ATCTGAAAAA AAATGGAATG
 13401 CTAAGGAGA GATTCATGTA CTTCTGAGAA CACTTTTAGC TCATTTTTTA
 13451 TAAGGCATCA ATATTAGATA GTTTTCTTGA TTAAAGAAAA AAAACACCA
 13501 CCCACTGCCT GCCTATATTT CTGGGTTGCA AATGATGGCG GTGGATGTGC
 13551 AGCCTCATCC GTGGCTAGAA GGCCAAATCC AAAGTCACCA GAGCTTGAGT
 13601 TTTTGTAGAG TTGAGATCTG TGTGTCAAAG GGAAGCCCT AGGGTGGTTC
 13651 TCTGCAGCAC CAAGAGCAGG GATTCATACC ATCATGTTCC TTTCTTTTTT
 13701 CTTTTCTCGT CTTTTCTTTC TTCCTTCTT TTTGTTCTCA TGAGTTCTCA
 13751 CTGTGTTGCC CAGGCTGGTC TTGAATATTT GGCCTCAAGT GATCCTCCCG

FIGURE 3A-6

13801 CATTGGCCTC CCCAAGTGCT GGGATTACAC ACTCAGCCAT GTTCCTTTCT
 13851 TCAAGTACGG TATTGACCCT TTGGCCACAG GAGAACGTGC CCAGTTTTTC
 13901 TTAAAGACCA CGTGGGAACT CAGCAGCCCA TGATTGTAGG TTCCTTTTTTC
 13951 CCTCATAGAG TGGCCTTCAA GGGCAGGTTT TTGTTATCTG CGTTTCAGAG
 14001 ACCCAAAGGG ACACAGGCAT TTCTGCTCCT GGAATTTTGC GGACTTTGAA
 14051 TCTTGAGCTC AGATTTTGGT CTCTGTTGGT TGCTTGTTTA TCTTCATCTC
 14101 TTGTCATTTT TGGAGCCTGC ATGCCTTCTC AGAGCAGCAG GTAAGTTGCT
 14151 TAGTTTTTTC ACATTGAAGC TGTGGCTGGG GGAAGGTAAC AGTGTCCCCT
 14201 CAGAACTCAT GGAGATGCCA GGCATAGTGG AGGCTGAGGC AGGAGGGTCA
 14251 CTTGAGGCTG GAGGATTGCT TGAGGCCAGC CTGGGCAACA TGGTGAGAGC
 14301 TCATCTCTAA AAAATTTTTT TAAAAATAAC TCATCAGGGG CTATTTCTTT
 14351 CATTGTATTT TCCTCTTCCT TTTGAACCCC TCTGCTGACT TGTTTCACTT
 14401 TCTTTTTTTC TGTTTGGTTT CTTTGAAGTC CTTTCTTCA TTATCATGTC
 14451 CTCATTCCCG TCCATCTTAG GTTTTTTCACT TCCTTGTTCC ACTCTCCCTA
 14501 ACCTGTTTCT GTGCCCTGTT TATGGCATGG CTCAGGATAT GAATTTTGAT
 14551 CTCCGTCTGA GATCTCCTTC AGGTATAGAA TCCAGACCA CCTGGTCTTT
 14601 TTGTTCTCTC ATTCCTCTGA TTTCTGTACA TTTAAGGATT CACTGCTTTA
 14651 GAAAACTTTT TTTTTTTTTC TTGTTTCTGG AGCCACCTCT CTCAGTAAAG
 14701 CCAGGCTTGG CAACTTATTA GGGACAGCAT TCTGGTTTCC CTGGTGACAG
 14751 GGTTTAAGCT GATTCTAGGC TGTGCTCTT AACCACATCAG GAATGCCATA
 14801 AGTATAGACC CTGTCTTGGG AGAGATCTGG AGAGATACTT GAGAATTTTG
 14851 GACACTGTAA TATTGAATTT GGTCTAATT GTGATCTAGA GACCCTCAGA
 14901 CTCTTTCAGG TGATGCACGA AGTCAAAATT CTGTTTCATAG TAACGTTAAC
 14951 ACAGTGTTGC TTTTTCATC TCATTCCCTC ACCAGTATAC AGTGGCATTT
 15001 TCCAGAGGCT AAATGATGTG TGGTAACATC ACATTCTTCT GGCTAATGAA
 15051 ATGTGTAATT CTGTATTCTT GTGTTTTCTA TAATTTTTTAA GGTAAGTACTT
 15101 TAAGGTAATA ATATGGAAGT TTTTATTGAT GGACTCAGTT TGTTCTTAGT
 15151 ACTTCTGTGC TCTTACTAGG TTTCTTCAGT TATAACTGCT ATCATCTTTT
 15201 TGTACACTTC ATTACTGTCT AATAAATCCT TATTTTGAAA TCCCAGCATT
 15251 TTCCTGGAAC CTTTGAGAAA ATATAAGAAG TAAGTACTAC TTGTAAAAC
 15301 TGCTTGTAAG AACTTTTGGG AAAACTCCTA ATTTTAAAAA TTTTATTGAC
 15351 AACTTATTTT AGCACTTTAT TCTAAAATAG AAAAAAATTT ATATTATTTT
 15401 TCTTATATGT AAGGGTGGAT TGTGCTTAA AAAAAGGGAG ATTAGAAGAC
 15451 TTGCTTTTTT AACCCATAGC TGCAACTTGT ATGTTAAAAA TACTGAAGTG
 15501 GACATACCAA CAAGTATAAA GGAGGACTTT AAAGAATCTG GGCAGAAGTG
 15551 TAAATAAGAA CTAAAAAAGG AAAAAAAGAA AAGAAATGAA AGTGTAAATGA
 15601 AAGCTACCTT CTCAGTTTCA TAAATGTTCA TAATGTACCT TACTGCGTCT
 15651 TATGCGACAG AACATTTTCA TGTAAGTATTA TGGTACCAGT TAAGTTGTGG
 15701 CATTCTTTCA AGATCATTTA GAGTTTAAAG AAAAAGGAAT TGCATATTTT
 15751 ATGCGTACGT ACTATGAGCT CTTTAAAGC CAAAATTTCT TCCAGTTTTT
 15801 AAAGTAGAAA TAAAAAAGTC ACTGAAGCCT CTATCTAACA GGATAAGTTG
 15851 CCACATTGCT TTGGCTGGAA AAGCCACAC AGAAACTGAG AGACGAATGA
 15901 AGTCTTGAAC AGCTGACATT CCTGAATGCC CACTGGATGA AAAGTCAGTA
 15951 AAATTCAAGG CAGTGCCGCT TTAAATGTTA CCAGGATTCA TTAAATTAAA
 16001 GATTTAGCCA GCGCGGTGG CTCATGCCTG TAATCCCAGC AGTTTGGGAG
 16051 ACCGAGGCAG GTGGATCACC TGAGGTCAGG AGTTTGAGAC CAGCCTGGCC

FIGURE 3A-7

16101 AACATGGTGA AACTCCTTCT CTAATAAAAA TACAAAAAATT AGCCAGGCGT
16151 GGTGGCGCAT GCCTGTAATC CCAGCTACTC GGGAGGCTGA GGCAGGAGAA
16201 TCGTTTGAAC CCAAGAGATG GAGGTTGCAG TGAGCCGAGA TCGTGCCATT
16251 GCACTCCAGC CTGGGCGACA AGAGCGAAAC TAAAAAATAA AAAAAAGATG
16301 TAGCTGCACA CATGAAGACC AAGTTAATAT CTTATTTACA GAATTTTACT
16351 TTCACCTTAC AAATGAGCAA ATCTATAGAT GTGGCTCGAC TTGCTGTATC
16401 AGCACCAACT GCTCATCAAA GAATAATTTA TTTTATGTGA ATGCTCAGCA
16451 GCAGATACAA ATGGTGATAA ATATTCAAAG GGTTGAATAA CTTCTGAAT
16501 CTCATGACTT ATCCTGGAAC AACTTTATTT CCATTTGCAC CCTTGGTGCA
16551 GAAGCAGTGG TGGAGAAAAC TGCTGACGCC GTAACATGGA TCAAGGAAGT
16601 GGCACTAAGC TCTACTAGTG GTCATTGTCA TGGTCTTCTT TCCCACCACA
16651 AACTTGTGGT TGAAAAATAA AAGCCATTTT TACTTGAGAA TGTCTTGAAT
16701 GAAGGATTAA AGACTATCAT TTTTTTTATT TACTTATTTA TTTATTTATT
16751 TATTTTAATT TTTATCTATT TATTTTTTTG AAACAGAGTC TCACTCTGTC
16801 TCCTAGGCTG AAGTGCAATG GCGTGATCTG TGCTCACTGC CACCTCTGCC
16851 TCCTGGGTTT AAGTGATTCT CCTGCCTCAG CCTCCCAAGT TGCTGGGATT
16901 ACAGGCACCT GCCACCACGC CTGGCTAATT TTTGTATTTT TAGTAGAGAC
16951 AGGGTTTCGC CACGTTGGCC GGGCTGGTCT GGAATTCCTG ACCTCAGGTG
17001 ATCCACCTGC CTCGGCCTCC CAAAGTGCTG GGATTACAGG CATGAGCCAC
17051 CATGCCTGGC CAAGACTATT AATTCTGTGT GTGTGTGTGT GTGTGTGTGT
17101 GTGTGTGTGT GTGAGGTCTC ACTGTGTGAC TTAGGCTGGA GTGCATTGGT
17151 GCAACCTCCG CCCACTGCAA CCTCTGCCTC CCGGGTTCAA GTGTTTTCTC
17201 ACCTCAGCAT CCCCAGTAGC TGGTACTACA GTGGGGATAC TCCACCCCAG
17251 GAGTGAAGCA TATAACCCAG TTCCNNNNNN NNNNNNNNNN NNNNNNNNNN
17301 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
17351 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
17401 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
17451 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
17501 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
17551 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
17601 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
17651 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
17701 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
17751 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
17801 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
17851 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
17901 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
17951 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
18001 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
18051 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
18101 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
18151 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
18201 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
18251 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
18301 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
18351 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN

FIGURE 3A-8

18401	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
18451	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
18501	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
18551	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
18601	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
18651	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
18701	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
18751	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
18801	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
18851	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
18901	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
18951	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
19001	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
19051	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
19101	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
19151	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
19201	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
19251	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
19301	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
19351	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
19401	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
19451	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
19501	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
19551	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
19601	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
19651	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
19701	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
19751	NNNNNNNNNN	NNNNNNNNNN	NNNNNNCCTC	CCAAAAAGGT	AGGGTTTCAG
19801	GTTTGAGCCC	CTCGCCACCC	GTCCTGGTTT	TTAATTTTTC	TCAATTTTTT
19851	CCCCATTTTA	AAATTTTCCA	AGGGTTTTTT	TTTTTTTTTT	TTTTTTTTTT
19901	TTTTTTTTTG	AGACAAAGTC	TCTCTCGCTC	TCTCGCTCTC	TCACTCTCTC
19951	GCCCAGGCTG	GAGTGCAGTG	GCGCCATCTC	GGCTCACTGC	AAGCTCTGCC
20001	TCCCGGGTTC	ACGCCATTCT	CCTGCCTCAG	CCTCCCGAGT	AGCTGGGAGG
20051	GACTACAGGC	GCCCCCACC	ATGCCCGGCT	AATTTTTTGT	ATTTTTATTA
20101	GAGATGGGGT	TTCACCGTGT	TAGCCAGGAT	GGTCTCGATC	TCCTGACCTC
20151	ATGATCCGCC	CGCCTCGGCC	TCCCAAAGTG	CTGGGATTGC	AGGCATGAGC
20201	CACCACGCCC	GGCCTAAATT	TTTCAGTTTT	TATACTCATT	TCCTTTTTGT
20251	TCGTTTTCTT	TCTTTAATTT	GTTAGTATTT	GTTGTTTTTT	GAGACAGCCT
20301	CACTTTATCA	CCCAGGGTGG	AGTGTGGTGG	CACGATGTTG	GCTCACTGCA
20351	ACTTCCACCT	CCCAGGTTCA	AGCAGTTCTC	CTGCCTCTGC	CTTCCCAGTA
20401	GCTGGGATTA	TAGGCACTTG	CCACCAAGTG	ATTTTTGCAT	TTAGTAGAG
20451	ACGGGGTTTC	TCCATGTTGG	TCAGGCTGGT	CTCCATGTTG	GTCAGGCTGG
20501	TCTCGAACTC	CTTACCTCAG	GTGATCTGCC	TGCCTTGGCC	TCCCAAAGTG
20551	CTGGGATTAC	AGGCATGAGC	CACCGCCCCA	GCCTGTTTTT	TGGTCAGCTG
20601	TTTTGTTTTG	ATTGCATTAT	AAGATTAGTT	CATCAGGTAG	ACTTCCTTTG
20651	GTATATATTT	AGTTGTGGTT	TGGAAAATAA	GTTTTTTATT	AAAAATAAGT

FIGURE 3A-9

20701 CATTATGTT TACATGTAAT GAGTTTACTC ATGTTCTGTT AAATGAATTG
20751 ATACATATTT AAATTTTTTCC TCACTTGAAT TTCTAATATA GTAAATACTG
20801 ATAGATAAAA TTCATATAAA CAAAAGCTTC TGGGTGTTCA GTTATTTTTTC
20851 AAAATGCAAA GAGTCCTGAA ACCAAAAACT GTAAGAATCA TGGTTGTAGA
20901 CAAAACCTGG TTTGGTTCTC CATGACTTTG GTTGATACAT TTTTTTTTTA
20951 TTTTTTTATT TTTTGAGACA AGTTCTCATT CTGTCACCCG GGTTAGAGTG
21001 GAATGGCATG ATCTCGGCTC ATTGCAGTCT CAACCTCCCA GGCTCAAGCA
21051 ATCCTCTCAT CTCAGCCTCC CAGAGTGCTG GGATTATAGA CATGAGCCAT
21101 TGTGCCTGGC TATATTATCA TCGTTATTAT TGTTTTGTTT TGTTTTTTGA
21151 GATGGAGTTT TGCTTTGTCA CCCAGGGTGG AGTGCAGTGG CACCATCTCA
21201 GCTCACTACA ACCTCTGCCT CCTGGGATCA AGCGATTCTT GTGCCTCAGC
21251 CTCCCAACTA GCTGGGATTA CAGGTGCACA GCACCACACT TGGCTCATTT
21301 TTGTATTTTT AGTAGAGACA GGGTTTTGCC ATGTTGGCTA GGCTCCTGGC
21351 TTCAATTGAT CTGCCTGCCT CGGCCTCCA AAGTGCTAGG ATTACGGGCA
21401 TGAGCCACTG TGCCTGGCCC TGTAATATAA TTTTACATGA GTTAATAGTG
21451 TAACATTTTC TCAGTTGTAA TTTTTTTTTT TGAGACAGTG TCTCACTCTA
21501 TCACCCAGGC TGGAGTGCAA TGGCACGATC TCCACTCCCT GCAACCTCCC
21551 AGGTTCAAGT GATTCTCCTG CCTCAGCCTC TTGAGTAGGT GGGATTACAG
21601 GCATGCGCCA CCACACCCGG CTAATTTTGT TACTTTTAGT AGAGATAGGG
21651 TTTTCACCAT GTTGTTGAGG CTGGTCTCGA ACTCCTGACC TCGTGATCCA
21701 CCTGCCTCTG CCTCCTAAAG TGCTGGGATT ACAGGCCTGA GCCACTGTGC
21751 CTGGCCAGTT TTAATTTTAA TACAATAAAT ATCAGTAGCT ATCACCCACA
21801 TGAAGAAAGC CATTTGACGT CATCAGTAAG AGTAAAGGGA TTCCAGACAG
21851 TGTGAGAACT CTTTTGTAAA CAGAGATAGG ACTGATAATC CCTGTCCTCG
21901 ATTGGTTGAT TACTTGCTAT GACCTCATAA TGAGCCTCTG TTTTGCAATT
21951 TCTGGGGCCC TGGCTGGGCC TCAGGAAGGC ACTTGCTGTC TTGGTTTTCA
22001 GTTGTCTAG CTGAGGAAGC TGGTTCTCAG TGACCTGATG GACCTTGGCC
22051 AAAGTTGGCT CATTTCTCCT TTTGAATACA TAGCATTACT TTATGTTTTT
22101 TTATTCCATT AAAAAGATCA TTTGGCTTAC TTGGATTTTA TTATGAGGTT
22151 TGTGTTTTAT TATGAGGTAG GTTTGTGTTT TTTTGTTTTT TTTTAACTT
22201 ATATGTTGGC TATTGGTCAG TTCCAAATTT GAAAACCTGCA ACGCTTACAC
22251 AGCTTCTATC CTTGAAGAAC CTTGGTGCCT ACAATAGCTG AGAGCTGGTA
22301 GGCTGCAGTC ACTAAGGCCA GACACTCAAT AGTCTATTCC CTGGGTGGCT
22351 TGAGACCTGA CATACTTTGT TTCTTTTTGT TTCTTTTCCT TTTGTACTTG
22401 ACTCTTTTTA ACCTGTTTAT TTCTTTTTTT TTTTTTCCC CGAGAAGGGA
22451 GTCCTGCTCT GTCACGCAGG CTGGAGTGCA GTGGCACGAT CTCGGCCAC
22501 GGCAACCCTC CGCCTCACAG GTTCAAGCAA TTCTCCTGCC TCAGCCTCCT
22551 GAGTAGCTGG GATTGCAGGT GCCCGCCAGT ATACCCGGTT AATTTTTGTA
22601 TTTTATAGTAG AGAAAGGGTT TCACCATGTT GGCCAGGCTG GTCTTGAATT
22651 CCTGACCTCG TGATCCACCC ACCTTGGCCT CCCAAAGTAC TAGGATTACA
22701 GGCACAAGCC CATGCCTGGG CTAACCCCTA TTTCTATCTT TCTTTTTTTT
22751 TTTCGAGACA GAGTCCCACT CTGTCGCCCC GGCTGGAGTG CGGTGGCCGG
22801 ATCTCAGCTC ACTGCAGCCT CCACCTCCA GATTCAAGCA AATCTCCTGC
22851 CTCGGCCTCC CGAGTAGCTG GAACTACGGG TCGTGCCAC CATGCCCGGC
22901 TTATTTTTGT ATTTTTAGTA GAGACAGGAT TTTGCCATGA TGGCCAGGCT
22951 GGTCTTCAAC TCTTGACCTG GTGATCCACC TGCCGTGGCC TCCTAAAGTA

FIGURE 3A-10

23001 CTGGGATGAC AGTCATGAGC CACCACATCC GGCCTCTAAC CCTTGTTTCT
23051 TAATGAAACA TACCTGTAAA CCCCACTGTT ATGTAGGTAT ACTTTATTTT
23101 TCCTGTAAGA GGTAGGTTTA TTTGGAGTGT TTGTAGCAGT GTGTGAACTT
23151 TGTATTTCTT TGACAAGTCC TTAAGTGACA GGGAAAATTG TAGTAGTATA
23201 TAATCTGTAA ACTACCCTGT AATTCTCAAC TTTGTTCTTT TGCATATACT
23251 CATTCTCCAA TTTCCATAGC ACCTCTAACT TTTAACAGCT TCCCTAAGTC
23301 CTACAAATAA TAGACCTTGG GCCTCCTCTA ATAGTCACTT TGACCAACTT
23351 TAAGCAAATC TTTTAAAACT CATGTGCGCT GGGTGCAGTG GCTCACTCCT
23401 GTAATCCAG CACTTTGGGA GGCTGAGGCG GGTGGATCAC GAGGTCAGGA
23451 GATCGAGACC ATCCTGGCCA ACATGGTGAA ACCCCGTCTC TACTAAAAAT
23501 ACAAAAATTA GCCGGGCGTG GTGGCGTGCG CCTGTAGTCC CAGCTACTTG
23551 GGAGGCTAAG GCAGGAGAAT TGCTTGAACC CAGGAGGGGG AGGCTACAGT
23601 GAGCCGAGAT CATGCCACTG CACTGTAGCC TGGGTGACAG AGACTCCCTC
23651 TCAAAAAAAA AAAAATAAAT AGAAATAAAA AAGCCAGGCA CAGTGGCCCA
23701 CATCTGTAAT CCCAGCACTT TGGGAGGCCA GGGCGGGTGG ATCAGGAGGT
23751 CAGGAGTTCG AGACCAGCCT GGCCAATATG GTGAAACCCC GTCTCTACTT
23801 AAAATACAAA AAATTAGCTG GGTATGGTGG CGCGTGCCTA TAGTTCCAGC
23851 TCTTCAGGAG GCTGAGGCAG GAGAATCACT TGAACCCAGG AGGCGGTGGT
23901 TGCAGTGAGC ATAGATCACG CCACTGCACT CCAGCCTCGG TGACCGAGTG
23951 AGACTCCATC TCAATGAAAA AAAAAAACA AAACAAAAAC TCATGTCATT
24001 TGCTCAGAAT CACATCTCAT TGGGAATCATT TTTTAAAC TGTTTAATCA
24051 AGTGCTCAAC ATATCAATTC GTGTCTACAT AGAGGATCAT AGCTCCATTT
24101 CCCATCACTC AGCAAGTCCC ATAATCTGCT TTTTCCACAA AGCGTATTTT
24151 TTTTCAGATT TACATGTGGC ATGCATTTCA GTTCCAGAAT TGAACCTAAT
24201 GTGCTATTTT CTCTCTTCGG CTA CTGCTGTCT GTGTGGAAGA TAAGGAACTT
24251 TAATTTTCGGG TTGGGTGCAG TGGCTCACGC GGGTAATCCC AGCACTTAGG
24301 GAGGCTAAGG CGGGCGGATC ACGAGGTCAG GAGTTCAAGA CCAGCCTGGC
24351 CAAGATGGTG AAACCCCATC TCTACTAAAA ATACAAAAAA CGTAGCCAGG
24401 CGTGGTGGTG GGCGTCTGTA ATCCCAGCTA CTCTGGAGGC TGAGGCAGAG
24451 AATTGCTTGA CCCCAGGAGG TGGAGGTTGC AGTGAGCTGA GATCGCACCA
24501 CTGCACTCCT GCCTGGGCGA CAGAGCGAGA CTCCGTCTCA GAAAAAATA
24551 ACAAGAATTT TAATTTCAAA TATTTGTTTA CTGTATTAGT TAAGGCAACG
24601 GCTTAGTAAT GGCACCTCCT GGATGGCCCT GTAAGCGCAT TAATCTGGTC
24651 CAAGTCATTG GGAAACTCAG CCTTAAAGGG AATGGAAGTGA GTGGTTGAAG
24701 AGTAGGCAGG GTCTCCTCAT TTTTGCATGG TTTGCCTCTG AGGCTGTGTA
24751 TCTTTAGCTA CAGACAGAAT AGCTAACATT TATTGAGCCC TACTCTGTCT
24801 GCAAGCACTT GTTTAGTTGT TTTACATTCA TTAACCTATT TACTCTTTTT
24851 TTTTTTTTTT TTTGAGACAG AGTCTCGCTC TTGTTGTCCA GGCTAGAGTG
24901 CAACGGCACA GACCTTGGCT CACTGCAACC TCCGCCTCCC GGGTTCAAGC
24951 AATTCTCCTG CCTCAGCCTC CCAAGTAGCT GGGATTATAA GTATCTGCCA
25001 CCATGCCTGG CTAATTTCTT TCTTTCTTTC TTTTTTTTTT TTTTGTAGAC
25051 GGTGTTTCGC TCTTGTTGCT CAGGCTAGAG TGCAGTGGCA CTGTCTTGGC
25101 TCACTGCAGT CTCCGCCTCC TGGGTTCAAG CAATTCTCCT GCCTCTGCCT
25151 CCCGAGTAGC TGGGATTGCA GGTATCCGCC ACCATGCCCC GCTAATATTT
25201 TGTATTTCTA GTAGAGATGC GGTTTTACCG TGTTGGCCAG GCTGGTCTCA
25251 AACTCCGGAC ATCAGGTGAT CCACCATCT CAGCTTCCCA AAGTGCTGGG

FIGURE 3A-11

25301 ATTACAGGCA TGAGCCACCA TGCCTGGCTT CATTTATTCT TTGTAAGTTA
25351 GTAGATCTCA CTGTTTTACA GGTGAGGAAA TAGAGGCCCA GAAATGTTGA
25401 ATAAC TTGTT TAAGGCTACA AACCCAGGTG GTCCAGAGTA TGTCAATTGTC
25451 AGAACCAGCT TTTCTTGTT GTGAAGAATC CTTTGTCCCT GGCTTCAGTT
25501 GTGTCCAGGC AGTAGAAGAT AGTTTCCTTA GGATTAGCTC CCAGTCAGTG
25551 TGAGGCAGAT GTCTTGACGC GGAATTTAGA GTCACAAATG GCCTCCTCTG
25601 CCTCCAGTTG TTTCTTTTGT CCTTGGTGGC CATTGGTAAA TGTGGCCGAA
25651 ATGGTGTGGA TGGAGTGGGA GCAGCTTTCT GGGCTCACCT CCCTACTATT
25701 GAGGGCTCTA CGCAAGAGCT ATGGGAGACC TTTTAAAGAA ACCCTCTTTA
25751 ACCCCAGCTT CTGATTCACA TCTTTATCTT TTCCCATCTT CCGGAATTC
25801 AAGAACCCCT TTAGAAAAAC CAAAGCCCCG AGTCCTAAAA TTGATAACCA
25851 GCAATTAAGT ACCTTAAAGT GTAGGGCATG ATGGATTTCT AGGTTTGACT
25901 ATCCTGCTTT GTGGCACCCA TGAAATGTTG GGATTCTAGA ACTCTTTCTT
25951 TGTAAGCACC CCACTCCCCA CCAAAAAAAAA CCCCACTAAA CATAAGAAGC
26001 TTTTGTCTGT GGATCTTAAC TGTGTATATT TTGTCTCTAG GAAGCAAAC
26051 CAGATTCTCT CTTACAACCG TCTGTGTGCC ACTTGACAC ACACAGGCAC
26101 AGAGCTACTT GCTTGTAGCC TTGACTGCCA GCAGCCCTGA ACACCGTAGC
26151 TGGTGGTGCC AGGCCTTGTG TGTGTTTAGG ACTTGCCAGT TCAGTCCTGG
26201 GAGCTGAAC CTGGACATCC TGCTGTGTGT CTCTTTATCC CATCGCTGGT
26251 GTAATTTATG CCACTACTTC CTGTTTGCAT TTGCTCAGTC TCTCCTTTGG
26301 TTTGCTTCTC TCTGCTGAAG CCGGTCCCCA TAGCTGTGCA CATGGCTAGC
26351 TATGGGGACT AGGCATCTAG ATATTCTAGA CATCTGCAGT TGTTTCTTAG
26401 TGGGAATGGT TGCTTTATGT CTCTCTACAG AATTTTAGTT GAACTTGAGT
26451 GTATGATTTA ATTTACTTGC TTGTCTAACT TCGGCAAGGG TGCCTTTTAT
26501 TTTAAGATGC CAGCATGGGG TGAGAGTAAA GGGGTGAAC ATTGCCCTCC
26551 CCCACCCCC CACCCCCCAC CCCCCCACTT TTTTTTNNNN NNNNNNNNNN
26601 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
26651 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
26701 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
26751 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
26801 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
26851 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
26901 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
26951 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
27001 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
27051 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
27101 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
27151 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
27201 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
27251 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
27301 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
27351 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
27401 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
27451 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
27501 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
27551 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN

FIGURE 3A-12

27601 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
27651 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
27701 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
27751 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
27801 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
27851 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
27901 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
27951 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
28001 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
28051 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
28101 NNNNNNNNNN NNNNNNNNTA TTAAATAAAT AAATAAGATT TACTTATCCA
28151 AAAGCACAAT TATGTGCTT TTTCTTTTC TTTTGAGACG AGAGTCTGAC
28201 TCTGTTGCC AGGCTGCTGT AGTACAGTGA CGCAGTCTCG GCCTTGACCT
28251 CCCAGGCTCA AGCAATCCTC CCACCTCAGC CTCCCAAGTA GCTGGGACTA
28301 CAGGCATGTG CCACTATGCC TGGCTAATTT TTTGCACTTT TTGTAGAGAT
28351 GGGGTTTCGT CATGTTGCCC AGGCTGGCCT GGAACCTCTG GCGTCAAGCA
28401 ACCTACCTGC CTTGCGCTCC CAGAGTGCTG GGATTACAGG CAGTCGCCAT
28451 TGTATCCAGC CCAGTTATGT AGTTATGTGC CATTTCTAAA CTACTTTAGA
28501 ACCCATCTCT TTGGTGTTG TTTGTTTGAG ACAGAGTCTC ACTCTGTCAC
28551 CTCAGCTGGA GTGCAGTGGT GTGATCTCAG CTCAGTGCAG CCTCGGCCCC
28601 CAAGGTTCAA GCGACCTCC CACCTCAGCC TCCCAAGTAG CTGGGACCAC
28651 AGGTGCTCTT TTTGTTAAGA GTGGAAAAGC CAAGGTCCAT GTACTTTTTT
28701 TGAGAAAGAC AGCCTGTTGG CTTTCTTCAG AGTGGTTCTG CCCCTTCCCG
28751 TACCCCATCT CCAACACATT TTTATCTCTC AACAGAGGTA GCTGCTATTC
28801 ACTCAGGTGT TCTTTAATGC TGTGGCCACG GCTTCCTTGG AGAGTGTGGC
28851 AGTGCTTTCC TTGCTAATGA AAAGGCTGTC ATAATGGGTT AGGTCCATAG
28901 GGGCTCTGCC CTTCTGTACT TGTATTCCA GGGAGAAAAA TCTCTACCTT
28951 AATTACCGAC ATCTCATGCT GGCAGAGAGG TGTGGTTGCT AATTGATTAG
29001 ATGACAGTCC TTTTCATTGA TGTGGCACTG TTGGGGTGGT TTTGTTGTGC
29051 TTTTCAAGT AAACAGATAG ATTTGGGCCA GGTAAGTTGA TTTTGAGAG
29101 ATGAAGTTCT GTGTAGGGAT TTCCCTTTAT TAAGCTCATG TCTTTAGTGC
29151 CACTTTTGTG TCCTGATTTT CTAACCTGAT AGTAAGAAGT ACTAAGTTGG
29201 CTTGTCTTGC TATTTTGGTG TGGGTGGTGA ATAATGTCTC TTCTACCCTG
29251 CTCTCTGGTG CGTTCCTGTT CTGTTTGGTA GCACCACATT CCTCTATTTT
29301 GTTTGGTTTT CATTCCCTCT TTCTCTCTTG TAATGGTTGG ACCCTATTCT
29351 GAAATATATA TTTTAAGATA GTGTTACTTT GGGTGGTCGA GGCGGGCAGA
29401 TCACCTGAGG CCAGGAGTTC GACACCAGCC TGGTCAACAT GATGAAACCC
29451 TGTCTCTACT AAAAATACCA AAATTAGCCA GCGTGGTGG TGTGCATCTG
29501 TAATCCCAGC TACTCGGGAG ACTGAGGCAC GAGAATTGCT TGAACCCAGA
29551 AGGCAGAGGT TGCAGTGAGC AGAGATTGTG CCACTTTACT CCAGCCTGGG
29601 CAATAAGCA AGACTCAGTC TCAAAAAAAA AAAAAAAAAA AGTAGTGTTT
29651 AAAAGCAAAC ACCCTGCCTT TTTTGAAACC ACAGAACTG CTTGTGAAAC
29701 AGCCGATAGG GCAGGCTGCC AAATACAGAC TGTAAAACC AATCTCTTAA
29751 TGACAAAATG TCAAACTAGT ATGTTAAACC TTCATTATGA CTGTGGTGTG
29801 AGGATTTTTT TCAATAAGAA ATGTTTAGGT GCTGAACTCC CAGTTTCACA
29851 TTCAGAATGC TTCTATTATC AAATCCTCT TGGTACATCA TTTCCGAGAG

FIGURE 3A-13

29901 GCTTGTGTAG CTAATCCACT ATCTACTGTA CAGGAAAGAT TTAAATAAA
 29951 CCTATTCCCA TTCATCCTCA TCTGTGTTTT TTTGTTTTTT GTTTTAATTT
 30001 CAAGAAGTAA TTTTCTTTTG AGGTGATTG GACCAACCGT CTCACTAGCT
 30051 TTTCCCATTT AAGATAGGAG AACTAGATTC AGAATTGTGT CTTTTTCCTA
 30101 ACAGAAGACT GGGGCCTTAA TCTTTACCCC CCAGGCTCTG ATTAAGTAC
 30151 TTTTCTTTTT TTAGATGGCA TAGAATCTTC TGTCTGTCTA GAGAATTTTG
 30201 TTTCTTGCCA GGCAGTGTCA GGAATTAGTA TTCATTCTCCTC CTGCTATCT
 30251 TCCTGAAGAG CTGTGAACCT GCTGGTAGCC TGATGGATAA GGGTACAGTT
 30301 GTTTGTTTAT TTATTGAGAC AGGGTCTCAT TCTCTACCCC AGGCTGGAGT
 30351 GCAGTGGCAT GATCTTGGCT CACTGCAACC TCCGCCTCTC AGGCTCAAGC
 30401 TATCCCCCAA CCTTAGCCTC CTGAGTAGCT GGGACCACAG TCATGTGCCA
 30451 CAACCCCAG CAAATGTTTT GCGTTTTTTG TAGAGACAGG GTTTCCCCAT
 30501 GTTGCCTTTG CTGGTCTTGA ACTCCTGGGC TCAAGTGATC CGCCTGCCTC
 30551 AGCCTCCTGA AGTGCTGGGA TACCAGGTGT GAGCTACCAC AGTTGGCCAA
 30601 GGTATAGTTT TATGAGCTGA GCTATAGAAC TGGTTGAATG GGAATTAGGG
 30651 AAAACAGACA ACCAATAATT GGAAGTAAA GGAAAAATAT ATAAGTGTGC
 30701 CTCCTTGGTC ACAGCTAGCC TTGTGACATT GGGGTTTTTG ATATAGAAGT
 30751 TCAGGAATCC CTTCCACCTC CTTCCCAAGA GAATTTCTTC TGTTGGTGT
 30801 GTAAGGGGCT TTTTCCAAC TCAATTCAT TACCAAGAGT CTTGAGTGGC
 30851 TTTATTTTCA ACTTGGGTTT TTTAAGCGCT TCTCATGTCA CCTTTGTTTG
 30901 TGTACTGGGC CTGTCTCAAG TTTCCAGAGG GAGATGAAAG ACAAGAAAAG
 30951 CTAAATGACT GGTTCTTCAG TGAGTTTCCC AGAGTGGCTT CTTCTCATTC
 31001 CAGCACTGCC TAACTCTCAC CATGGCTGAC GCCGTGGGCA GGCATCCGCA
 31051 TTCATGGAAA GCCAGGTCCT AGCTGGAAGT GACACAGGGA TCTTCAGATC
 31101 TCTCTTAGCC CACTGTTCTC CTGAAAAAAA AACAAAAGCC ATAGACAGTA
 31151 AATTGGGGGA ATAGGCTGAC CATAACTTCA GTTCGTGGAT TTGGGTCCCA
 31201 CACTGGATTG TGTGATTTGT GCTTATCTCC TACTAGATTG TTACCTTCTT
 31251 TGAAGGCTGG ACTGTATCTT ATCCTTCTCT GTATCACTTC GGACACCCAG
 31301 AAAGTGTGG AGTACTTTGC ACATGGTCAC CTCTTAATGA ATTATTTGTG
 31351 AAACAAAAT TTTTTTAAAT TGTAACATGA GGCTGGGTGT GGTGCTTAG
 31401 GCCTGTAATC CCCGCACTTT GGGAGGTAGA AGTGGGCAGA TTGCTTGAGT
 31451 CCAGGAGTTT GAGAACAGCC TGGGCAACAT AGCGAAACCC TGTCTCTATA
 31501 AAAAATAGAA AAGTTAGCTG GGTGTGGTGG TGCGGGCCTG TAGTCCCAGC
 31551 TCCTTGGGAG GCAGAGGTGG GAGGATTGCT TGAGACCTTG TCTCAAAAAA
 31601 ATAAAAAATA ATTACTTAAA AAAATCGTAA CATGGGTATT CTCCATTACA
 31651 GTTACCCTTA GGAAGTGTG TCCATATTGA TTTGTAAGTC TGATATCAGT
 31701 CTATCTGATT CTTTGGCTGT GTAAGTCACA AGTCTTAACC AGTATCTTAA
 31751 GTAGGTGTGG TAATGACTAC AGAGAAGTGC TTTTTCAGGA TGAGAAGATG
 31801 AGGGAGAAAA TTTACACCAT TGCTGGATTG TGTTAAGAAC TCGGAGAGGA
 31851 AACCACAGGG AGGATGCACT GCTGAGGAAA TCGTCTGGCT TCCTGGAGTG
 31901 GGGACCAGAG CCAGAGAGCC AAGCCCTCCT GGCTTTGCTG AGTTCTGTCC
 31951 TTGCCCCCTGA CACCAACGTG TCTGCCTGCT TTGTTGCTCC TGGTTACAGT
 32001 GGGCTCAGTC TTGCCTCTTT TTTGATGGGT GGGCAGAGGA AACTAGTGT
 32051 TGGGAATATT GTCCAGCGTT GGAGAGATCA TGTGGTCTGT CAGAAGGCTG
 32101 GAGTTATTTA TAGTGGGAGA AAAGCCCAGG AGCATGGCAC GGAAGAAGT
 32151 GATTTACAC CAGCTCAGCG CCTGATGATG GTGAGGACCC AGATTTTCTC

FIGURE 3A-14

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32201 TTGAGCATCT CAGAGCAGAT CAGTCGCTTT TCCTGATTGA CCCATGAACT
32251 GTGAGACTAG GGACCATGTT TTCCGAGGCC ACTGTGAGTG AGGGAAGAGT
32301 GAGAAGGATG ACCATTTTCT TCTTCCTTGA TTCTGGTCTT TGTGATGTGT
32351 GGTATGAAAG TGTCATCTGA CTTTTGAATC TCCTTTTATT GAACTGGTGA
32401 AGAAGGCACC AGCTGTGTGG GGTGGTGGAA ATAAGGACCT GTTAAACTGG
32451 TCTGCCTGTA TCTGCCTCCC TGCTCCCCC TCACCCACC CACCCACC
32501 CTGGGCAGGG AGGCTGAAAC TGCTGCTTGC TAGGCTTTGC CAACTCAGTT
32551 TCTCTTCATG GATTACCTGC TCGCGGCAGG CAGGCAGGCA GCTCCCCACC
32601 TGGAAGCCTG CAGACTCGCC GAGCTGAGAG AATCATGCTG CAGGTGGGGG
32651 CAAGTGCTAG GAACTAGGTG TGCCACTTAC CTTAACAGGA GCTGTGCCTA
32701 GTCCGGGCTG CTCAAACTAA GGCTGCAGAG CCCTGGGGCC TGTTGGAAAT
32751 AGACTGTGCC TTTCCCTGCG CCTTGTTGGC ACATTTTAT GGTATGTGGA
32801 GAGTCTGGGA GGGGCCGGGA GCTTGTAAT TGTGAGTAA TGAAGTCTAG
32851 GGAGGGAGAT GATCCTTCTT GAGGGCACCC TGAGTTCAGG GTTGTCTGT
32901 TTCTGAGGTG TGCTACTGCT TAGTACCCTG ATTTCTGGAG TTGTCTACCT
32951 AGGTTGCTTT TAATTTTTC AGCCTTAGGT GGAAGAGATT TTCCATCTTG
33001 GTGTTTAGGC ATGTTAGGTG AGGTTTACTT CCGGAGCCAG ACTTTTAGGC
33051 AGGTTGTCTT GACATAAGTC AAGGTCAGGA AGCGATCTTC AGGACATGCA
33101 GACGATGCCC ACTTCCTGCT GTGGTCTTGA AGAGGGCTGG AAGGCTTGTG
33151 AGCACAGAGG CACTGAGGGC TGTCGCATCC ATACAGGAAG ACACTCAGGG
33201 CTCGTCTCCG GTGCCTCATT TTATAAGCAT GGAAACAAAA GTCCCAGGAG
33251 GGTGAATGAC TTGCCCAAGG TGACATAAAT TGTTTGCGCA GAGCTGGGTC
33301 TAGAATGGAT CTTATGCCCT TGGCAGCGTG CCCCATTGC CATCACTTCA
33351 GAGGGGCTGG CTGCAGCCCT CAACGGCAGA AGGCAAGCTG GGAAAGGACA
33401 AGTGGAAGGG TAGCAGGCCC CAATTCTGCA CACTGGAGAG CACCTCTGAA
33451 ATCCTGCCGG AGACTATGCC CATAGAGGTG CCAGAGGCCC TAGGGAATGA
33501 TGATTTATTT TGTATTTTGT ATTTTGTGG AGACAGGGTC TTACAATATT
33551 GCCCAGGCTG GTCTCAAATC CTAGGCTCAA GTGATCCTCC CACCTGGGTT
33601 CCCAGAGTGT TGGGATTGCA GACATGAGCC GTGGCGCCCG GCTGGGAATG
33651 ATTTAAAAGT CGGCACCAGC ATTCTAGCCC TGACCCAGGC TAAAAGGGGT
33701 CACATGGAGC AGAGCTGTGC AAAGAGCTTT TGGGTGAGGA GTCACCTCCA
33751 GAAAAGCGAG AAGACTCTGA CCCCAGACT TCCCGTGGTG AGTTAGGAAA
33801 GCATTTCTGG AGAGCCTGTT AGGTGCCAGG CACTGTGGCT GGGCACTGAA
33851 GACACGAAGT GATTTAGTCT TGGAAATTCC CTTATGCTGC TCTCAGTCTG
33901 TGTAATAGTG AACAAGACAG CCAACAAGAG TTGTGAAGGA GGCCGTTGAG
33951 CAAGCAATGA AGTGCTAGTG CAGGAAGGCC CGAGCTGGGA AATGTCCGGA
34001 GAGACCCTGT GAAGTGATGC AGGGATCAGG AAAGCTTCCT GGTGGAAGCA
34051 ATGTCTGAGC TGAGGCTCAC CACAAAGAGG AATGGGAGTG ACTGCTAGAG
34101 GGAAAGTGTT CCAGGCAGTG GAAAGCTGTG GCCAAGACCT GGGGGGTTCT
34151 GAGAGGCCAT TGTACATTTG AAGACAGGTG GCTGGAACCC AGAGTGAGAC
34201 TCTAGGAAGG GAAGAGAGTT AGTCTGGAGC TGCAGGCAGG GAAGGGGAGA
34251 CAGCCAGCTC ATAATACAGT GTGGGCAAAA ATCCAGAAAC CATGTGGATC
34301 TAATTTGATA TCAATTTTAC ATGTATATGT GTATATACCT ACACACACAT
34351 ACATAAAATC AGTTATGTTT GTGTGTGTGT ATATGCATAT TTGTGTGTGT
34401 GTGTACGTGC GTGCATACAG AAAGTTGTTT TTTTAAGGCA TGCTTTAAAT
34451 ACGAAGCCAT CACTTCCTTT TCCCAGTCCT GGGTGCTTT TGAGATGAGT

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FIGURE 3A-15

34501 GTTGGTGCTC CCCCCACCGC CATGTGCCAT CTTCTGGAGT AAGAGGGAGT
34551 GCTTTCACTG TGTGCAGGTG TGGCTAAAGA GTATTCAGTG TGTGCAGGTG
34601 TGGGTGAAGA GTATTCACCG TGTGCAGGTG TGGCTGAAGA GTATTCACCG
34651 TGTGCAGGTG TGGCTGAAGA GTATTCAGTG TGTGCAGGTG TGGCTGAAGA
34701 GTATTCAGTG TGTGCAGGTG TGGGTGAAGA GTATTCAGTG TGTGCAGGTG
34751 TGGCTGAAGA GTATTCAGTG TGTGCAGGTG TGGGTGAAGA GTATTCAGTG
34801 TGTGCAGGTG TGGGTGAAGA GTATTCAGTG TGTGCAGGTG TGGGTGAAGA
34851 GTATTCACAG TGTGCAGGTG TGGGTGAAGA GTATTCAGTG TGTGCAGGTG
34901 TGGGTGAAGA GTATTCAGTG TGTGCAGGTG TGGGTGAAGA GTATTCACAG
34951 TGTGCAGGTG TGGGTGAAGA GTATTCAGTG TGTGCAGGTG TGGGTGAAGA
35001 GTATTCAGTG TGTGCAGGTG TGGGTGAAGA GTATTCAGTG TGTGCAGGTG
35051 TGGGTGAAGA GTAGGCTGTC CAGGATTTCA ATCCTTGGCT TTTGCTCTGC
35101 AGCAAGGGCT GGCTGAGGGC ACTGTGAGGC TTCTTCAGGC CCAGGAGTCA
35151 GGCCCACTTT CCCTTTTCTC TTGAGGGAAT GACTCAGAGA AACTCCTGTC
35201 CACCGGAGGT TCTGCAGGCT TTTGAGAGGC AGCCAGTGGA GGCTGATGGT
35251 AGCAGTTGGT GAGAAAGAGG AAGTATGTAG TGGCCATTCC TCCGGCCACT
35301 CCTGACAAAT ATTTCTGTCA CTAAACAGCA CCTCTCTGTG GCAGCCTTGG
35351 GCTGTGTTCT GGAAAGGGAG GAGCTTTCTC CTCCCTGTGG GAGGGCCTGT
35401 CATCTGTGGC TTCTGCTTTG CCCTTGGCCA CAGACTAGAT TGCACAACAC
35451 AGCCAATGAG AGTCCCTCTT CCCTCACAAG TGCTTGGAGT GCAGACCTTA
35501 ACTTACAGGG TTGTAGAAGT GACCGTGTTC CACACTGCAG GGTCCAGGTC
35551 ACAGCCGGCA AAGCACATGA AAATTGACCT AAGGTTAGAA TGTGATTATC
35601 CTA CTGGGAA AGGTTTACTG GGACAGCATT TCACTTCTGA CTCCATAGGC
35651 TGTGCTCTCC TGCCAGGGAG TGAGTTTTGT TTCCATGCTT GTCCAGTCTT
35701 TACTGCTTTC CCAGAGGCCA TAAACCTGCC TTTTCCCAGA GGCCATAAAC
35751 CTGCCCACCT CCTGCTATGT TCTAGTTCTG ATAGGAGTAC CATTGAGAGT
35801 TCTTGGCAGG GGACCAACCC GCTTCTACCG TGGTTGGTTT CCCCTCCTTT
35851 TCCCAGCTTG TTTGATGTGC AC GTTCTCCA AAATTCTTAT GCAGCTGGTT
35901 GGCTCTGTAG TGCCAGAGA TTGGAGCTCC TGCAACGGGA ACCCCGCCGC
35951 TTCCCTCCCT GGTTTTAGGG GCAGGGCTTG AAAATAAAGA ATCATAATCT
36001 CCCTCCTCCT TCCTCCTCCT CTCCTCCACT TCTCCCTGCC CCCACCCCA
36051 CCCCCACCC CACCCTGCCA GGCAAAGTGG AGTGACCAGC TCAGAGCGGG
36101 ACTCAGTCCA CCTCCCTGCT CTGCATGTCA GCAGTGATCT GGAGGAGATT
36151 CCGGGGCGCA TGAGTATGTG AACTCTGGAG CACGTTACTG TCCCAGGCTG
36201 GCACTCTGTG GCAGGTGTGT GCACTCATTG TGCTGTTACT GGAGACCAGT
36251 CTCCTTAGGG GTGATGGTGA CCCAGCTAGA TGTCTGCCAG GTCTGTCCAA
36301 GGCCACCCTG TTCTCTAATA GCTTGGGAAA TGGAAAGCAC TTCTAAATAC
36351 CCCTGCTCTT CAGAAGAGCT GGCTGGGTGG TTTGGGGAGT TTCTTCTTTG
36401 AATCTCTTAG AGTACAATAT CCCTTTTTTC CCGAAAGCCA GGTTCCTTAG
36451 TTCCTAAGCT CCATTCTCTT GTTGCTAACT TACTACCTTC AGTTTTCTTA
36501 GGTTGGGTGC ATCTTCCCTG GCCTCAACAA GACAGTGGCT GAAAGGTCAA
36551 GAGAGTGGTA GCTGCTCCTT TGAGAGAAAG GGGATGTTGG AGTGGGAGCA
36601 CAGGCTGCCA GCAGTTGTTT CACCTTCCCC CTTTGGCTGG CTAGGAAAGG
36651 GGCACCACTT TAGTCTTCTG CCAACCTCCA CAGCCAGCTG TGGGAAAACC
36701 CAAAAGGAAA CATCCTCTCG CTGCTAAGAC TTGAGAGCCT GAGGCAGAGA
36751 CCAGCCAGTA GCAGCCCGAC CCTGCTGAAT GGGGAGGATT GTTTATTTTA

FIGURE 3A-16


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36801 TTTTATTTTT TTCTGAGACG GAGTCTTGCT CTGTTGCTCA TGCTGGAGTG
36851 CAGTGGCGCG ATCTCGGCTC GCTGCAACCT CCACACCCCA GATTAAAGCG
36901 ATTCTTCTGC CTCAGCCTCC CGAGTAGCTG AGACTGCAGG CATGCGCCAC
36951 CACGCCCAGC TAATTTTTGT ATTTTAAATA AGAGACAGAG CTTCAACATG
37001 TTGGCCAGGC TGGTCTTGAA CTCCCGAACT CAGGTGATCC GCCTGCCTCG
37051 GCCTCCCAGG GGACTGGGAT TACAGGCATG AGCTACTGTG CCCAGCCTGA
37101 AGATTGGTTA TTTAGGGGCT GTGACAAATG GTTTTGCAAG GGAGCACTGG
37151 AAAGCCTGTA ACTTCACAGA GCCAGGGGTC AGCTTTTGTG CCATAGCCTT
37201 ATAGCTTCTG TGGCCTGTAG TGCCTGAGGC CAGGGGATCA GGTGCTGACC
37251 ACCTTTCCCT CTTCTTCCT GTGTCTTGCG GCCAGCGACT GTTATTGTCA
37301 GGTTGACCCT CTGGTTAGAG AGGATGACTT TGGCCTGGTG TCCAGACTCC
37351 CTGCTGCCTT ATCCCCTCTG CCCTGGAAT GCACCTAAAA ACAATTACTT
37401 TCCTCCTGAT TCCAACATAA GTGGTCACAG AAAGTTCTGT TTTGGCATT
37451 TGATTTCTGA TTGGGAGTTT AGGCATCTGA GAATTGAATG CTTGCTTTAT
37501 ACAAATATAC CCTTAAGACA TCTCCTCTTT TTTAGCCCTT ACATGCTTTG
37551 CTTGGGTATT AATTGAAGTT GGGGCTTTTT AGGGACCTTA TGTGCTTAC
37601 CTTCTAGTT TCCCCTCCAC TCCACCCCA AAAAACCCAA AGAACATTGG
37651 AAAAATTGAG CAGTGCCTCA AGGTCATTG ATCATAAGTG GTATTTGGCA
37701 TAGTTAACTG GTTTGGTGTT TGGTGAGAGA TTTCTGCTTT ATATTTGAGC
37751 AAAAAATTTT TTGGCGGGAG GCCTCTATGC TGTGTTGCCA ATGCTTGCCC
37801 TGTGCGCAGG GTTTGCCCCC TCCCCTCCCT TGACAGGTTG TTCTAATCCC
37851 CTTGTCTATA AACAAGTGCA GCAGAACTTG TCGGCCAGC TCACATGACC
37901 TTGGTTATCT CTTTAACCAG CATCAGCGTT AGATACCACG GTCATTGAC
37951 ATGGTAGAGC TGTCAGGGTA GAGTGGAGAT ACCAGCAGGA ATCCTGGTCC
38001 ACGAAGAAAG GTAAATGGGA GTGTGTGTGA GGCCTTAGGA CTGGGTGGGA
38051 AAAGTCTGTT CCCATGGGGT AGGGCTTTCA GCTGTGAGAA GAGGATAATT
38101 TCATTCTTTC TCCTTTTTTA AGAGACTGTC TCACTCTGTC GCCCAGGCTG
38151 GAGTGCAGTG GTCTAATCAA GGCTCACTGC AGCCTCAACT TCCTTAGCTC
38201 AAGCAATCCT CCTGCCTCAG CCTCCTGAGT AGCTGGGACC ACAGGTGCAT
38251 GCCACCATGC CCAGCTAATT TTTTTTTTTT TTTTTTTTTG AGGTAGAGTC
38301 TCACTCTGTC ACCCAGGCTT AAGTGCAGTG GTGCGATCTC GGCTCACTAC
38351 AGCCTCAGCC TCCCAGGTTT AAGCGATTCT CCTGCCTCAG CCTCTTGAGT
38401 ACCTGGGATT ACAAGTGTGT GCCACCATGC CCAGCTAATT TTTATATTTT
38451 TAGTAGAGAT GGGGTTACAC CATGTTGTTT AGGCTGGTCT GAAACTCCTG
38501 ACCTCGTGAT CCGCCCACCT CAGCCTCCCA AAGTTGTTGG GATTACAGGC
38551 GTGAGCCACC ACGCCCAGCT AATTTTTCTT GTTTGAGATG GGAATCTCA
38601 TTATGTGGCC TAGGCTGGTC TCGAACTCCT TGCCTCAAAT GATCCGCCTA
38651 CCTCAGCCTC CCAAAGTGCT GGGATTACAG GTGTGAGACA CTGTGGCCAA
38701 CTTTCATTCC TTCTTTATCA CCCTAAAATT TCTAGTTCTG GCGTCTTGTT
38751 TATCTTTCTC AAATCCTGTC TGCAGGGGCC CAGGACATGC AGCTGTTTCA
38801 GGAAACCGCC CTTGAGATGG GGCAGATGTA TGCTAGTTCA TGGGCTATAA
38851 AACTCAACAC CAAAAATCCC ATCGTCCTAA ACAGTGACCT GTTATGTTGT
38901 GTGAAGGACA GTGGCGATGG GGGCCTGGCC GCCAGAGAGG CTGCTGGATT
38951 CTATGGCAGA CACACTCAGG AGCTGGAAGT GTGGCTAAGC TTTAGCAGC
39001 ACCATCACTT CCCTCCCCAT ACACATGCAC ACAGGTTTCC TTTGTCTCAC
39051 AGCTGAAGAG GCAGCGCCCA GCTTCAGTAA GCACTGTGTA TGAGAATGGA

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FIGURE 3A-17

39101 CTTACTCTGG CCACACTGTG CACACGCATG TGTGTGTAAG AACTGATCA
39151 CATTTCCCAT AAAGACTGTT GATTTGCAGA GTTCCAGGC CCATACATCT
39201 AGGGCGGGAT GTGTGTGTTT TCATCAGGGG AGAGTAGAGT GGCCTTTTGT
39251 GGAAGGGATA AAATGGTTGA GCTGCTGGAG ACTTTTCTAG CTCCATTTAT
39301 ACAGCAGCCT TTCTGCCTGG GTGCAGACTT GAACCCAAGT CCAAGTTCAA
39351 GCCATGTGTG TAGATGACCA GAACTTAGCC TTCAAACCTA GCCTTCAACT
39401 TCAGGACTCT CCTGGAGAAA ACATCCATCT CCTTTTGGAG ATACAGAGAA
39451 TTCGTGATGA GCTTTGAGTA CAGAAGTTCA AGTTATATTT TCTGGCAACC
39501 TACAGAATAA GTTGGGAAAG GATATGTAAT TATAGAAATA ACCAGCATGT
39551 CGCCAGGCAT TGTGTCCGT GCTTTAGATG GTGTGGATAT TTTGTAATTT
39601 CTGATTCTTT ACCTACTGTT TTCAAGACTT GGTAGGGACC CCGTTATGGC
39651 TGTGGGGTTC TTTGTCCTTG GTAGTTAGCA TGAAGTATGT AGAGCAACAG
39701 AATGGGTAGC CGTGGCCTCT GGCCACCCAG CTAAATTCTA CTGATGAGAG
39751 GTATCCTGGG TGGGTTTCTT CTTTGGGTCT TCGTTTATGC CGCCATTCTT
39801 ATTGCCAGTT AGAGCTGCCT TTTAGGATTT GTTGGGTAGG AGCTGTATTC
39851 CTCTTGGAGC CATCTTTTCT TCCCTGCCAT CTCTGAGTGA ATTCAGAGGT
39901 GGAGAGCTAC AGACTTGGCT GCTTGCCTCC TTCAAAACAC CCAGCATTEC
39951 CTTGTCCACA GTCTGTGTAG CAGCACATCT AACAATGCCC AAAAGCGGCC
40001 CCCTTCCTCC CAGCCACTTG TTAATGGGTG GTTCTGGTTC CTGAGGGCTT
40051 CGACCACTGC ACGAGCTAAT CTCAGTGAAG AGTGCCATTC CCAGGTTTCT
40101 ACCACAGAAG TTAGAAAGCT CAAAGCCCAG GTCTTCTGCA CCGAAGAGTG
40151 CCATTCACAG GTTCATACCA CAGAGGTTAG AAAGCTCAAA GCCCAGGTCT
40201 TCTGCTGCCT TGGGCCATTC CTTTCTCTTA GAAACCAGTT CAATCAGACT
40251 CTTTTTTTTT TTTTTTTTTT TTTTTTTTGA GACGGAGTCT TGCTCTGTCA
40301 ACGAGGCTGG AGTGCACTGG CATGATTTCT GCTCACTGCA GCCTCGACCT
40351 CCCCAGGCAC AGGTGATCCT CCCACCTGGG CCTCCTGAGT ACCTGGGACT
40401 ACAGGTGCCC ACCACCACGC CTGGCTGATT TTTGTATTTT TAGTAGAGAT
40451 GGGGTTTCAT CATGTTGGCC AGTCTGGTCT CGAACGCCTG ACTTCAAGTG
40501 ATCCGCCCCG CTCAGCCTCC CAGAGTGCTG GGATTACAGG CGTGAGCCAC
40551 TGCACCCAGC CCAGACTCTT TTCATAGGAT GCTGAAAGGA TGAATTAAGT
40601 ATAAAAAGTG CCTTTTGGCC AGATGCAGTG GTCATGCCT ATCACTTGAG
40651 AGGAGCTTGG GCAACATGGT GAAACCCCAT CTCTACAAAA AATACAAAAA
40701 TTAGTTGGGC ATGGTGGTGG GCACCTGTAG TCCCAGCTAC TCAGAAGGCT
40751 GAGGTGGGAG GATCACCTGA GCCTGGGGAG GTCGAGGCTG TAGTGAGCCA
40801 AGATCGCGCC ACTGCACTCC AGCATGGTGA CAGAGACCTT GTCTCAAAAA
40851 AAAAGTGCTT TTTAATAAGG TACACGTAAT GGAAAATGGC TGTCTCTGG
40901 TTTGCCATAC TCTGCTCCTA GGTAGAAAGT ACAAACAGCA AGGGCCCCTT
40951 GGAGCAAAAT TGTCAATGCC GCCAGTGAAT AAACAGCAGT GGTTGGCTTT
41001 GAGGGGCACC TTCAGCCTAA AGCCATAAGC TGACATATAC TCAGTCTCAC
41051 TGAGAAGCTC GGGCTTTCCA CTGTTACCT AACTGCTGAC AAATGAATCC
41101 TCCATTGATC TGGCAAGCTG GCCAGGATAC CTGCCCAGGC CATGGCCACT
41151 TAGTAACAGG ATCCGGTTCT CAGTGCAGGG TTGAGACTGC AGCAGCAGTG
41201 GCAAGCCAG TAAGGCAGGT ATGAAGCACA GCCCCCGCAT CGGTTGCCTA
41251 GTAGGAAGA CAGTTGTAAG GAGCATTTGC CCCTGTTATG TCAGGGTACT
41301 GTTGCAAGTT GTCTTTTCTC CTCTAGCTGG AAGTTGTTCT ACCCAGTCTT
41351 CCTTAATTAG CTCTCTTTT GTGTAAGGCA GCACCCATTT AAAATTCTTT

FIGURE 3A-18

41401 TCCTCCAGCC TCATTCCTCA TCTCCATTG GGTATATATC TCCTCAGAAC
 41451 CTCTCTCCTA CCCAGCCTTA AGCTCTACCC CAAATGCTTT GAAGCTCTCT
 41501 TGTTCAAGTC TTTTTTTTTT TTTTTTTTTT TTTTGTAGAC AGAGTCTCTC
 41551 TCGCTCTGTC GCCTAGGCTG GAGTCAGTGG CACGATCTCG GCTCACTGCA
 41601 AGCTCCGCCT CCTGGGTTCA CGCCATTCTC CTGCCTCAGC CTCCCCGAGTA
 41651 GCTGAGACTA CAGGTGCCCA CCACCACGCC CGGCTAATTT TTTGTTTTTT
 41701 TAGTAGAGAC AGGATTTTAC CGTGTTAGCC AGGATGGTCT CGATCTCCTG
 41751 ACCTCGTGAT CCACCTGCCT CGGTCTCCA AAGTGCTGGG ATTACAGGAG
 41801 TGAGCCACCG CACCTGGCTC AAGTCTTCTT GATTCAAGCC CTCACCCAGA
 41851 GCTTGAAGAC TAGGGAGCCC CCGTGTCTGC TGCCCATGGT GCTTGGAGAG
 41901 CAAAGATCTG TTCCCGGGTC CTGAGTTGGA ACTCTGAATT CATTTCTCTG
 41951 TCTGGGCTAT GGTTTAAGTC TTAAGTACAA TTCACGTACC CCTTGAATA
 42001 CTATGCTGGG ACCTCATGGG CTGGCCTGAG AACACAGCTA CCATTTGTAA
 42051 CATGTTTCTA TGGAAAAAGA GTTCCTTCTT AGAACAGAAC TTTTGGTAAC
 42101 TTGGGGATTT CTTGACTAAT ATGCTGCAAC AGATTTGCAT TTGCCTGTGG
 42151 AAGTGTCTCT TTATTTTGTA TTCAGCTGGG CACGGTGACT CACGCCTGTA
 42201 ATCCCAGCAC TTTGGGAGGC CGAGGCAGGC AGATCACTTG AGGACAGGAG
 42251 TTTGAGACCA GCCTGGCCAA CATGGTAAAA CCCCATCTCT ACTAAAAATA
 42301 CAAAAAATA ATCTGGGCCT GGTGGTGAGC GCCTGTACTC CCAGCTACTC
 42351 TGGAGGCTGA GGCAGGAGAA TCACTTGAAC CCAGGAGGTA GAGGTTGCAG
 42401 TGAGCTGAGA TGACACCACT GCACTCCAGC CTGGGCGATA GAGTGAGACT
 42451 CTGTCTCAAA AAAAAAACAT TTAATAATC ACATTTTGTG GTCATGGCAC
 42501 TATCTATCAC ACAAGTAAGT TGTCTCTCTA TATGCCAAAT GACAGAAAAG
 42551 AAGCACCTCT CTCTTCCAC CCAGAAAGGT TGCTAGAGAG CTACCCTTGT
 42601 CTTCTGTGAT TGCCTTGAGG GGCAGGTTTG TCTGGGTTCT CCATGTCAGC
 42651 TGATTTGATC CATAGTCCAG TAGCACCTGA AACAGGATGC CCTCATTCCA
 42701 CAACTTAGGT GCCCTCTCCT GCTTGGTTTT TTAATGATCT GCTACAGGAG
 42751 AAAGATAGCA CCTCTCCCTT CAGCAGGAGC AGCCCAGTAA GGGCTTGCTT
 42801 CTAGAAAGAT TGGCCAGTTG GATTTTTAGT GGTCACCTAA GTGGAGTAGC
 42851 CACTTTGCAG CCTGGCCCAA CAGGGAGACA GTTCTGAGGT GAGGGTGGCA
 42901 GTGACAGCCT TGGGGTGGTT TCTGATGTGC TCTGACCTCT GGCCATGGTG
 42951 ACTTCTGGAG CAACAACTT TGTCCCAGTA TTTTTTCTG ACATTTCTCT
 43001 CTCCTTATTC AACTCCCTCT TTGAACTGG AGGAGTAGGG AGGCAGTATT
 43051 TGTTCACTTC CAGAGAAAGA TGCAGCAGGA AGAGGCATAT GTCTTGTCTT
 43101 GCACTTTCCA GCAGCAATGC TGGGACTAGG GGGTCTAGAA GGCCTGTTTC
 43151 CCAGCTCCAG GCTGGATCTT ATCCTCAGCA TACAAGCAAG TTTTAAGGAA
 43201 ACAACATTGG AAAGGGCAGA AACAAAGGGT TAAATCTGTA CCCAGGTAGA
 43251 AAGACTGTTG CATAAATGCT GAGTTTTTTT TTTGTTTTTT TTTTAAGAT
 43301 CTCATGCTTC TTTTTTACTT TGTGTTGGCA AAAACCCAG GAGAAGATGG
 43351 GAGATTCTGG GAGGAGATGA TTATGCTGGG TGAGTCAACT GAGCTCCCCA
 43401 GCTGCCGTTT TTAGTTCTTT TGCTTTTCTG TAACAGGAGG CAGTTTGGGG
 43451 AGGGGTGGG GGCAGGGTGG GAATGCTGAT TTTTGCAGCA GGACAGGAGG
 43501 CAGGTGTGTA TGGGTGAAAT TATTTTGACA CCCTAGAGTT AACCGGGCCT
 43551 TAGAGTCAGT ACATTGGTTC AAGTAACAAA TATCAAAGCA GAACTCTTAG
 43601 TGTGGCAAAC AATAAATAAT TGTCTCCTAG ATTCTTATAC AAGTCACTGT
 43651 CCGTCCCCAA TTGGTAGCTC TTAGAATGGC TCGAGTTGCA TTCATTGTCA

FIGURE 3A-19

43701 CAGCAAGACA CAATGGTTTT GATAGCAAAG CAGTAGAGAA ACTAAATGTA
43751 GAGAGGCAGA GAGAACTGTA TTAAGTCTGA GGACCTGGTG GTTGTCTATGG
43801 GCAGCAGGAA GTGTGAAGGA GAGGGTTTTT CCTCCGATGA AAGGAAGGCT
43851 AGGGCTTGAT TCAGGGGAGC AAGTGGGATG GGCCCTGCTG GTCCCTGGCT
43901 GTGCCTATAT TCTGAGTCTG TCTCCAGCTC ACCTTGGTGA TCACTCACTT
43951 TTCATCCATC ACTGGGATAG GGGATCTCGT GGCTCATTAC CCTCATGGGT
44001 ATTTTTTGCA GAGTACACTG AAGTGGGCTA TCAGTTATCA GTTGGTCCCA
44051 GAGACCGTCA TGAAGACATC GCAAAATGTT TTCTTATGTA TTCATTTGTG
44101 CACATTTATT AATTCAGTAC TTTACTGAAT ACTGTGCTGG GCATTGTTCT
44151 GGGCCATGAA TAAGACAGAC CTGGCCTGGT GCAGTGGCTC ACGCCTGTAA
44201 TCCCAGCACT TTGGGAGGCC AAGGCAGGCA GATCACCTGA GGTGAGGAGT
44251 TCGAGACCAG CCTGGCCAAC ATGGTGAAAT CCCGTCTACT AAAAAAAAAA
44301 AACAAATTAG CCAGGCATGG TGGTGGGCAC CTGTAATCCC AGCTACTTGG
44351 GAGGCTGAGG CAGGAGAATC GCTTGAATC GGGAGGCAGA GGTTGCAGTC
44401 AGCCGAGATC ACGCCACTGC ACTCCAGCCT GGATGGCCAG AGAGAACTC
44451 TGTCTCAAAA AAAAATACCA AGGTCCCTCC TTTTGTAGTG TAGTCTAGCA
44501 GGAAGGACAG ATAGTAACCA ACCAACTTCA AGGGCAACGA ATGCCTCGAA
44551 AGAGGGGAAA TGGGGCTGGT AGCAAGAAAT TGTGATCTTC CTTCTCTAC
44601 CCTTATCTCT TGGGGTCGAG AGTGGGGTCG AGAGTGGGCA ACTTTAAAGA
44651 TCAAAAAGTT GTGCCTCTCT TGTTCCCTAA GTATTGTAAC ATGGGTCAGC
44701 TAGGTGTGGG CACTGTTGGG CACTGAGGGT ATATGAAGGT GAGGGAGATA
44751 CTGGCTCTCA TCTGTCAGAG CATGAGGGGG TTAAGGTATG GGGACACAAA
44801 CAAGAAATCA ATGGGGCTGG GTGTGGTGGC TCACGCCTGT AATCCCAGCA
44851 CTTTGGGAGG CTGAGGCAGG AAGATTGCTT GAGCCTAGGA GTTTGAGGCC
44901 AGCCTGGGCA AGATGGCAAG ATGCCATCTC TACAAAAAAA ATGAAATAAA
44951 TAAAAAACTA GCCAGGCATA GTGGCACACA CCTGTAGTCC CAACTATTCTG
45001 AGAGGCTGAA GCAGGAGAAT CCCTTGAACC CAGGAGTTTG AGGATGCAGT
45051 GAGCTGTGAT TGTGCCATTG CAGTCCAGCC TGGGCAAGAG AGCAAGACTT
45101 CATCTCACAA AAGAAGAAGA AATGAAGAGT ACAGATAGAG CGCTGAGAGT
45151 CTAGAGAAGT GAGTCTAGAG AAGTGAGTGA CCACTCCCCG CTAAGACGGT
45201 GTCTGGATTT GAGATAAACA ACGGATAAGA GGACTTACCT GGATCACAGG
45251 AAGGCGCATA GGATAGATGA CCACTTTCCT TTTAGTATGT GTAGATCTGG
45301 GTAGCTCTTT GTACCACAAT TCTGACCCAT TCTTTTTTCT TATTATTTTT
45351 ATTTATTTAT TCAAAATAAT AATTTTTTTT TTGAGACAGT CTTGCTCTGA
45401 GCCACCATGC CCAGCCTGAA ATAATAAAAG TTTTAATCTT TAAAAAATA
45451 TGGGCCAGGC TTAGTGGCTC ACACCTGTAA TCCCAGCACT TTGGGAGGCC
45501 GAGCTGGGCG GATCACCTGA GATCAGGAGT TCGAGACTAG CCTGACCAAC
45551 GTGGAGAAAC CCTGTCTCTA CTA AAAAATAC AAAATTAGCC GGGCATGGTG
45601 GCGCATACCT GTAATCCCAG TTA CTGTTGGG GGCTGAGGCA GGAGAATCAC
45651 TTGAAACCCG GGAGGCGGAG GTTGCACTGA GCCGAGATCA CGCCATTGCA
45701 TTCCAGCCTG GGCAACAGGA GCGAAACTCT GTCTCAAAAA AAAAAGGAAT
45751 GCTTCACAAA TTTGTGTGTC ATCCTTGAC AGGGGCCATG CTAATCTTCT
45801 CTTTATTGTT CCATTTTTTT GTATATGTGC ATGTACAGAG TAGTGGAGCT
45851 GGGTTATCAC TACAGTCTAA CTCCAGAATG ACACCTTCA CTA CTATAACC
45901 ATATATGGTG CCCAGTATA CAGCAGTGA GCTAGGAAGA AAAGCCCAGT
45951 GTCTAGAGAG CCCAGAAAAT ATGCCAAGAA CATATATACT AGGCAAAGAA

FIGURE 3A-20

46001 AACGAGGTTA GGAGGAAGCC CAGCCACCTC AGCTGCACTG GTTAGGATCT
46051 GCTGCCTCCC CACAGTCCTC TGTAAGTGA GCCAGACCTC TATGCTGCAG
46101 GCTTCCTTCT GCCTACCCCC ACCACCCCCA TCCCCCAGAG CCCTGGGCTA
46151 CTGGCAGGCT GGCTCTCCTG TGATATGGAG GAACTTGTTG GTCTCCATGG
46201 TTACG GTAAC CCACTGGTAT GGGAGGAACC GCATAAAGTG CGAGGCTGGC
46251 AGTGTGAGCT TCCCTCAGCC CTTGGCACCA TGTGGTACTG GTATGTCGGC
46301 TGTTTCATGG ACCTTTTCTG GGAGGAGGGA GTTAAGGAAC TGATGAAGAA
46351 GGAAGAACC CTGGCAGGAC CACTGTCGTC ATCCTCTGGG CCACACAGAG
46401 GGCGAAGGCA TGGGCACCAT GTCATTGAGC TACTCCTCCT GCAGGATGGT
46451 TTTATGTTAG GAAAGAGGGT CCTCTTTGCC TGATTGCCCC GCCATGGCAG
46501 AATTTGACTT TTCCTTGTTA TAGAGGGAAT ACCAGGATGA CAGGAATCAA
46551 CTTAGCTATA CTGGTACTTA CAGTCAAATT TCTAGGTATT GTAGCTCTTC
46601 CCAGAGCCCC GAGAACCCTT GGAGAGGGGA AACAATGGTT CCTACCCAAA
46651 AATGAAGCTA GATAATAATA GAATACATCA TCAAGACATT ACTGAACACC
46701 ACGTTCTATG GTAAACACTG ACATGGATT TCTTTTTTTT TTTCTTTTGA
46751 GACAGGGTCT TACTCTGTCA CCCAGGCTGG AGTGCAGCAG TGTGATCAGC
46801 GCTCACTGCA GCCTCAGCCT ACCTCCCTGG GCTCAGGTGA TCCTTCACC
46851 TCAGCCTCCC AAGTAGCTGG GATTGCAGGC ACTTGTCACC ACACCCCGGC
46901 TAATTTTTGT GTTTTTTTGT AGAGCCTGTG TTTTGCCATG TTGCCCAGGC
46951 TGGCCTCGAG TTCCTAGGCT CAAGGGATCT GCCTGTCTTG GCCTCCCAAA
47001 GTGCTGGAAT CAGAGGTGTA AGCCACCACG CCCGGCCAGA TTTTCTCATT
47051 TAATCTTCAC TCTAATTCTG TGAAATGGGT ACAGCTAGTA TCTTTATGTC
47101 CCAAATGAGG AAACAGATTT GGAGAAGTTA TGCACTTTG CTCATGTTCA
47151 GTCAGCTGGT AAGCAACAGA GGTGGGCAGA GCGACTATAG TAAGTTTTCT
47201 GTATAGTTTA CCTCTTCTAA GTTCTTGAA GGCAGGAGCC AGATCGCACT
47251 GAGCTTTGCA ACTGGAGCCA GGGCTCCAGA GTACTGCTCA ACAAAGGTTT
47301 GCTAGGGCAA CAGTAGCTGG GGATTTAGCG ACCAGACCCC AGCAAGCAGA
47351 TTCTCAGGGA TGAAAGTAGT CCTGGAAGCC TCTAAAGCCC TGGTTGCTCA
47401 GTAGAATCTA GTTTCAAGAG GAGCCCAGCA TTTCAAGTGG CTCTGAAGAC
47451 AGAGGAGATT TGGAGAGTGC TCTTTGCATT GTGGCTTCCA GGCCTGAAGG
47501 AGAGTGAGCT GGAGGTTGCT CTCTGTTCTC ACCTCTTATG CCATGTCAGG
47551 TTTTCCCAG GCAGGCTTGA GTCCTGGGGG AGCCCCGCCT CATGGCCCAG
47601 GCTGCAGTGC TGATCTCCCT GCCTTGTTGGT GAGGATTGCA GCTCAGAGAG
47651 CTAAAGGGCA GTAAACCACC TTGGTTTTGG CTTTGTGCTT AAGTTGCAGG
47701 CTCTTCTGGT TATCCTTTGT GAAGGAGGCT CTTACCCTGG CTGGAAAGAG
47751 GGAGCAGCCC CTGCCTCCA TCTACAATGG GACAGTAAAG GAATATGGCT
47801 GTTCTCAAG TGAACAGTC ACAGTTAATT TTGGGGGTGG GAGCATCCAG
47851 GCTTTCCACT GGTGAGTGCC TGCCAGTTTT ACAAGCTCTC CTACACTGAA
47901 TGCTCCTCTG GTTTATTGAC TCTTGCGAGT TGATAGCGAT AGTTGCTCAT
47951 GGCAGTTGAT AGCGATAGTT GCTCAGAATC AAAGGATGAA AAGACAGTTT
48001 CTGGATACAG TGAGGGAGGA AGGGTTAAAA AACAAAGGAC TCCAACCTCC
48051 AGTTACGAGA TGTCCCATAT GGCCATGCGC AGTGGCTCAC TCCTGTGATC
48101 CCAGCACTTT AGGAGGCCGA GGTGAGAGGA TTGCTTGAGC CCAGGGAGTT
48151 CGAGACCAGC CTGGGCAACA TGGAGAAATC CTGTCTGTAC AAAAAATACA
48201 AAAATTAGCC GGGCTTGTTG GCCCATGCCT GTAGCCCCAG GTATTCAAGA
48251 GGAAGATCAC TTGAGCCCAG GAGGCGAAGA TTGCAGTGAG CCAAGATCGT

FIGURE 3A-21

48301 ACCACTGCAC TCCAGCCCGG GCAACAGAGC AAGACCCTGT TAAAAATAA
48351 ATAAATAAAT AGGGACTTGC CACAGGCACA TGACCTTTCT TAAGAGACAA
48401 AGTCTTGTGC TGGGAATGGT AGCTCATGTC TATAATCCCA GCACTTTGGG
48451 AGGCCAAGGT GGGCAGTTCA CTTGAATTGT TGAGTTCAGT ACCAGCCTGG
48501 ACAAGCTTGC AAAACCCCTAT CTCTACAAAA AATACAAAAA TTAGCCGGGC
48551 GTATTGCTGT GGGCCTATAG TTGCAGCTAT TCGGGAGGCT GAGGTGGGAG
48601 GATGGATTGA GCCCAGGAGG CAGAGGTTGT AGTGAGCCAA GATCGTGCTG
48651 CTGCACTCTA GCCTGGGTGA TAGAGTCATA CCTTGTCTTG AAAAAAAG
48701 AGAGGCTGGG CGTAGTGGCC CATGTCTGTA ATCCCAGCAC TTTGGGAGGC
48751 TGGGGCGGGT GGATTACTTG AGGCCAGGTG TTCAAGACTA GCCTGGCCAA
48801 GGTGGTGAAA CCCCATCTTA CTAATAATAC AAAAATGATC TGGACGTGGT
48851 GGCACGCACC TGTAATCCCA GCTATTTGGG AGGCTCAGGC AGGAGAATCA
48901 CTGGAACACA GGAAGCGGAG GTTGCAGTGA GCCGAGATCG CACCACTGCA
48951 CTCCAGCCTG GGTGACAGAG CAAGACTCCA TCTCAAAAAA AAAAAGAGGC
49001 CGGGTGCACT GGCTCAGACC TGTAATCCCA GCACTTTGGG AGGCCAAGGT
49051 GAGCAGATCA CAAGGCCAGG AGATCGAGAC CATCCTGGCC AACATGGTGA
49101 AACCTCGTCT CTAATAAAAA TATAAAAAA TTAGCTGAGT GTGGTGGCGG
49151 GGCCTGTAA TECCAGCTAC TCGGGAGGCT GAGGCAGGAG AGTTACTTGA
49201 ACCCGGGAAG CAGAGGTTGC GGTGAGCCGA GATTGCGCCA CTGCACTCCA
49251 ACCTGGGCAA CAGAGTGAGA CTCTATCTCA AAAAAAAAAA AAAAGAGACG
49301 AGAGTCTAAT TCTGTACCC AAGCTGGAGT GCAGTGGCAC GATCATAGCT
49351 CACTGTTACC TCCACCTCCT GGA CTGAAAC GATTATCCTG CCTTAGCCTC
49401 CCGAGTAGCT GAGACTACAG ACCCATGGCA CCATGCCTGG CTAATTTTTG
49451 AATTTGGAGA GAGAGGGTCT CACTCTGTTG CCCAGGCTTG TCTCGAATTC
49501 CCAGGCGCAA GTCGTCTTCC CACCTTGGCC TCCCAAAGTG CTGGGATTAA
49551 GGCATGAGCA ACAGTGCTCA GCCCCGTGTG GCTTTTTTTT TTTGAGACAG
49601 AGTCTCACTC TGTTGCCAG GCTGGAGTGC AGTGGTGCAA TCTCTGCTCA
49651 CTGCAACCTC CACCTCCCAG GCTCAAGCAG TTCTCATGCC TCAGCCTCCG
49701 AGTAGCTGGG ATTACAGGTG TACGCCACCA CGCTCAGCAA ATTTTTGTAT
49751 TTTTAGTGGA GATGGGGTTT CGCCATGTTG CTTAGGCTGG TCTCGAACTC
49801 CTGACCTCAA GTGATCCACC AGCCTCGGCC TCTCAAAGTG CTGGGATTAC
49851 ATGGTGGGGG CCACCATGCT TGGCCCCCAT GTGGCTTTTA ATCTAAATCC
49901 TACCCTATCT CTTCCCAGCT TTTCTGTTT TAGTCAGTGC TTTGTATTTT
49951 CTCAGTTTAC AAAATCCCTT ACTGTCTCCC ACAAATAGGA TTGAGGAAAC
50001 AGTCCTTCTG TCACATTGCA AAGCCCTAGA AAAATGAAGG GACTAGAAAA
50051 ATGAAGCTGT TTGATCCTGC TCTGGTTCTC AGTCTACCAG TGAGTGAAGG
50101 GCCGGAGGGC CCGGGCAAGC TTGAGCCCAG GATCCAGTGG GCCCACTGAA
50151 GTCAGGGCCC ACTTTTGGGG GGCTGGGAAA AGGAAGGGTT GCTGTGGGAC
50201 CACTGGGATA GGCCTTTAAA CAGCACTTCA CCATTGGCCT GAATCAAACA
50251 TTGTCAATCC CAGTGTCCCG AGCACCTTCC CTGAGTCTTC ATACCTTCTG
50301 CCTCCTAGCT TATGGAGGAG GAGCCAGGGG CTTATCTTTT GGGGGAAATG
50351 AGAGCACGAT TAGGCATCAA GAAGGGTTGA TGAGAACTG GTAAGGGGGA
50401 CTGTCAAGAA CAGCAGAGTG CTGAAATGGT GACAAAAGCT CTGGGCTCCG
50451 GCCCCAGCTC TGTACTGAGA AGCTGTGAGA TTTTGGGCAA GTCTCATAAC
50501 CTCTGAATGC CAATTTCTCA ATGGAACACA GGGAGACTAC CTACCCTATA
50551 GGTCTGTGTT TGGAGAAAAC AAAGTGTAAG CGCTGGACAT ACAGTAGCAT

FIGURE 3A-22

50601 CAGAAATGCT GAATCCGTTG GCCAGGGCTC ATGTGTAAGG CAAACATTTTC
50651 TTGGCCACTC CTGAGTAGCA TGGTCTTGCA GGAATATATG CTTAAGTGCT
50701 GTGAGAGCAC AGAGGAAGCT TTGCCCTTCC CTAGAGGGTT AATGGCTACC
50751 AACGTGAGAA GGTACGAGG TTCCTTAATG AGAGGGAGCC TAGCCTAGAA
50801 TAGGGGATGA ATGAGAAATT GTTCTGAGAA CCAGAGGCAA GGCTGCAACC
50851 AGCACATAGA CAGGGGTCGT TGGTCTAGAA GGGGAGTCTT CTCCAGATGA
50901 GAGACAGCCA GCTTGCCCTG TGCTCACCAT GTGCCCAGAT AGTGGGGGCT
50951 TAGCAGGAGG AAGGTGTGAG GAATCCCAGG CCTTTGGAAT TCCTTGAGAA
51001 AGCAGTGTTG TTTTGAAGGT AAGGCAGGGG ATTGGTGACT GGAAACTTGG
51051 AGGTGAGTGA GAACCTAGGG ATGAACGTTT AGAAGCAGGG CTGGAAGGAA
51101 CTTAAAAGGG ACATTTGGAT TGTTCCTAGC TTTTGGGCAA AATCTAGGAT
51151 TAAATATGAT TTTTTCATTG ATAGAATGCT CTATCAGTGA TAAAGGCTCT
51201 TAATCTAGAA AACATACACC TCATAGGGGG CTTTACAGAG TCCCCAAACT
51251 CCCTGAAATT ATGCTCAAAA TATTTTGTGT CTAAGTGGAA TGTGCATGTT
51301 TCCAAGGTTA AGCACTGCTT TTTTAGGAAG TAGGAGGTCC GTCCGCCACT
51351 GTCAGCTTGC TGGTTTCTGC TTACCCTCCT CCCCCTTCG TTCTTGAGGG
51401 GGTGGTTTGC TGGTCTTTGG CAGGGCCGCC ACTCTGGGTC AGCACATCTG
51451 AGTCACACAT GTTCCTCCCC AGCCCTATTG GAGGCTTTGT TAAAGTCATC
51501 TGCCCCCTACC CAGGTCCAC CTGCCACAGG TGAGCTAGGG TTTTATGACA
51551 GCCGTGGCTG CAGTGAGTCT CCTCGACCTC TCGCCAGCTG TTACCCAGCA
51601 AAGCACCTTG GGGAGGGTGG GGCTGCCAC TTCCGGGGAG GGAGGGAGGG
51651 GGAGGGGAGA AGGAAGTTGA TCTAAACCCG CCTCTTTCTC TGTCTCCCTT
51701 CCTGCCCTAT TCCCCTCCTG CCCCTTCCCT CCCACCTTGC TTCTGGTGTG
51751 CTGTCCTGGA ATTGCACGCG CTTCTGACC ACCAGGCTCT GGCCCTTGAG
51801 AAGCCAGCGG GGCTTTGTCC CTGTTGCTCT CCTTGCCAAA CCCAGTCTCT
51851 CTGCTAGTGG TGGTTTCGGT TGCACACCG TCCAGGTTCC CAGGCAGGAA
51901 CCGCTCGGCC TGGCTGCTTA GCTACTTTTC ACTGAGGAGG TGGTGAAGG
51951 TGTCGCCTGC TCTGGCTGAG TAAGGGTGGC TGGCTGAGCC GGCAGCCCCC
52001 GCCCTAGGCC TGGCTCTTCC CGGCCTCTGT ACTTTGCCCT CGCTGCCTGA
52051 CAGGTTCTGC TGTGGGCTCT GCTGAATGGA AGTCGCTGGT AGTCCTTTTC
52101 CCTTCTCCA GTCGGGTATG TTGTCCCCCT TTTTACTCTA GGATTGCCTC
52151 CTCCTCTTTC TTTCTCTCA TCTCAAACAT AGGATCTTTA GAGAGTTGCT
52201 AAGGGGCGCC CTGCCTGAGT CCAGCATAGT AATATTCATG GGAAGGGTGT
52251 CCAGATGTGG AAGAGGCATT GACTAGGAAA GGAAGAGGGG GCACATACCA
52301 GAAGGGTCTC CCCTGAGAAC AAGCAGCTTG ACAAGTGGGC GAGGAGGGGC
52351 TGGTGGGAGG CAGAGGCCTG AGGCCTCAGA GAGGATGCTC CCGTGCTACA
52401 GTGAGGGGGA GCCTAGGATC TGGGGCCATT GCCCAGGACT GGTGCCCAAG
52451 GGACACTTTT CTCCCCAAC TCTATAGTGC CTGGCTTACT CTGCTTCTGG
52501 CCAGGGAATA TCACCCCTCC TGGTTTGGCT CTTCTCAGC CCTCGGGAAG
52551 CCAAAGGACA CTTGAAGCCA GCCCTGAATG CAGAGCCCCA AAGCATGAGC
52601 TTCTCCATGG GACAACTGTT GGTAGGAGCC TCCAGCATTG GGGCAGGGGC
52651 CCTGCCTACC TGAGTCAGCG CCAGGCCTCT CGGGGTGGAG GCTGTCTTCC
52701 GGGCAAGCCT GACAACACAC CTAGGCCGAG TCTGAGATCC CAGGCGGAAG
52751 GGGCCTGACA GGCCAGTGG ATGCAAAACT ATCTTTTAT TTTCTCCTCC
52801 ATGTCCTGCC TTCTCTCTTC CTCTCAGTAG CAGACCCCAA AGCTGTTTCA
52851 GCCCTACTTC TGAATCAGGC CTGCTTAGTA ACTACTTGGT TTGCCTTTTG

FIGURE 3A-23

52901 GTTCCAAATA ACTGCCTTGC AGGGTGACCC CTTATTCTTT CTAAAGGCTA
52951 CTTGAGAGCC ATAGGGTCTA CTCTTGACAG ACCTCCTCCA TCCTTTAGGG
53001 CCTGTCTAGA GTATGATATA GGCCAGAGCT TTGGGAGTGC CTGGTGTGCC
53051 ACGTCTTACT ATAAGCAGGG AGGATGGTGG TAGAGGGGAG AGCGTGGCTT
53101 TTGCCAGGTC CTATTGAGTT GGCCAGCAG GGCAGCTAAT CCTCAGCCTG
53151 CCATCCTGTT GGTGAGACCC AGGGCCAAGC TGAATGGTGC AGCCAGAACC
53201 AAAAAAGAGA AACTCTCTCT CCATATTAGC CACTGCATAC TCTTACCTCT
53251 TTATCCTTCA GGAAGAAGC TAGGTGAGGA AGTTGCCTCA CTTGGGGCCT
53301 TGGCCCAAGA AGCATTTCTG TTGGAGACTC TCTCCTCTCT TTTCCCTTTT
53351 TCTTTTCTCT GCTTCCTTCC AGTGGCTTGC CTCCTTACCC TGGCTCACAT
53401 CCCTGCTGTG GGAAACATCT TACAGCATAG AAGAAGGGGT GCAGGGGTAA
53451 GTAAGGGAAG GATTGAGCAC TTGGAGTCCT CTGAGTTGGA TGGTTCAGTC
53501 CCGAAAAGGG GGTGGTGAC TTTGGAGCAG GGGATCAAAG AGCAAGCACC
53551 AGTGCTTGTT GCTTCTCTGG CTCCTGAACA AGCAGAACCT CCTCTCTTTC
53601 CCTGTCCTGG ATACCCAGCG TGGGACCAGC CTTTACAGC CACCCTGTCT
53651 TGAGTTCCTG ACTCTCCTCC TTCCCTCTTT TGAAGGCTAG AGGTGCTGGT
53701 GTCGGCTAGC AACAGGTTGA GGGAGTGTGG CATTTCACCA GGTCTGGAGG
53751 AGAGCGGGCA CTCAACCTGG CCCCTTCTGC GGAAAGGCCC GTAGCATCTC
53801 TTGTCAGCCT TCAGCTGAGC TGTAGCTGGC TTAGCGGGCT CAACTTCGAT
53851 TTGGAAGGTT GTTTTGACAG TGAGACTTCT GGATTGGCAG ACAGTAGTAT
53901 TTGGGGACAT AATGATTGCT CTTATTGAAC ATCGGATAAG GCATTTTACA
53951 TGTGCTCTTT CATCTACCTG TGTAAAGTAG GGAATGTTTA TTGCCACTTT
54001 ACAGATAAGG AAATTAAAGC TTGTACGTGG GGGAGCCAGG GCTTGAACCT
54051 GATTCTGTTG GACTGCAGAG TTCCTCGGGA TCCTCCCTGG CACAGATGTC
54101 TGGCAGTATT GGCCACTGGT CGTTTTTTGG GTAGTTCTCT TCCCCATTG
54151 TAATAGTCTC ACCTCCTTCT TGACAATGTT GATGTTACAC TTGTTTTATT
54201 TTGGGGCTTT TTGTGTTGT TTGTGTGTGT GTGTGTGTT TCCTTTTTGT
54251 GAATGGGGGT CCACTGTAT TGCCTTTTTA AATATATTCT TTTTTTTTTT
54301 TCCTTTTTGT GAACAGCAGG TCTTGAATC TTGGGCTCAA GCTATCCTCC
54351 TGCCTCTGCC TCCCTAAGTG CTGCCTGTAA AGGCATGAGC CACTGTGCCT
54401 GGCTTGATGA TGTTGATGAT AATAATAAAG TTAATATGTG CTGAGTAGGT
54451 GACAGATTTA GGATTTGAAA CCTGGCAGCT TATCTCCGAC ATCTACAGTC
54501 TTAACCAGAA AGGAAGAGAA TGAATGGTAC AATCTTGCTT GTGGTTGTTA
54551 AGCTCCTTGA GGCCCACTTG TGCAGCAGGG CCAGGCAGGG AATGCTGACC
54601 TGCTGTGCCA CACAGACCAG CCCCTCGGTT CACCAAGAGG GATGGGCAGA
54651 GCAGAGCTCA GGATGGGCAT GGGATGCCCA GATTTGGTCT CAGTTGGCAA
54701 AAGGCCCAAG TCTGCAGGTA GATGCTAAAT CCCTGGTCTG GATTTTGAGA
54751 ACTTAGAGAC CGTCACACTT CCTGCTGCCT TGGGCTTATA TCCTCGGAGA
54801 AACAGGGAGT GACAACAAAC TTAGAAGGTG AACTAGAGGT TGCCAAGGAA
54851 ACTTTCCAC CCATCTTCCT CTCGTAGGAG TTGGGGCAGA AGGAAGGTTT
54901 TTTCTGTTC ATTGCCGTT AGGCAGATGG GTAGGGTTGG AGGCAGTCTA
54951 GCAGACTGA AAGGGAGGAT GGGGCTGAGA AAAAGGTAGC CTGAGGAGAC
55001 CAGGCTTTCA GTACCCTGCT GGACAGGGCT AGGGTACCCT TCAGGAGGCT
55051 GGCCCAATCA GGTGCCAGCA GGGCCTAGAA ATGCCCTTCT CTCCAAGGGG
55101 TGTGAACCCT AGAGTTCCTT TGGAAGGGAA AAAAGCAGGT ATTTAAAAAT
55151 CCACTTGTCT TGCAGACACT GTTTGAGGAC CAACCAGGCT TAGGTGAGCT

FIGURE 3A-24

55201 ACAGGGTGCG TGGAGAACAG AGCACCAGAG AGCTCTGTGG GCTGGAATGA
55251 GCAGACAATA AGAGCTGGGG GGCTTCATGG AGATGCAAAG GTTGATGAGG
55301 AAGAGAGAAG GAAGTTAAAA GGGCCTCTTC TGGGATGTGA GGAGCCTCCC
55351 CCTTCAAACA TCTACCAAAT GCATGGGATC TTCCTCCTCC AAGGTCCAAC
55401 CCCATGTGTT TCTGGGATCT GGTCAAACAG CTCACCAAAA GACAGCCTGC
55451 AGCTACCATG CAAAGGCCCT ACGTGGGCAC AGTGAAGAAG GGGAAATGTC
55501 AGAATCAGGA TACTGTACTT AACTTGCTGC TGTCGTTTCT GCCTGAAAAG
55551 CATCTGGTTG AGCTAGCAAG CTTCTTGTCT AGGAATGCTG GACAGTTCCT
55601 TGGGTAGTAG CAAGTCATTC TTTTTTCTC TGTGGTTTTT GAGTGCTTCA
55651 CGTACAGCCA GCAGGGGCCA TGAAAGGAAG AACTTTCAC TCACTCCTC
55701 TGGTCACCCT GCTGCCCTCC AGACTGTTTC CTTGAAGTTT CCAAGGCAGC
55751 TCTGGATGGT TCTGGGATGA GGCTCTGGCC TCATATGCTT TGTTCAGTA
55801 TGCTGGAGCG ATCGCTCCAG ATGTTCTTTG TGAGATGTAA ACCAGGGCGC
55851 TAATCAGGAG TTAGACCAGA CTCTGCATTT TTTTTTTTTT TTTTTTGAGA
55901 CAGGGTCTCG CTCTATCACC CAGGCTGGAG TACAATGGCA TGATCATGGC
55951 TCACTGCAGC CTCGAACTCC TCCTGGGTTT AAGCGATCCT CCCGCCTCAT
56001 CCTCCAGAGC AGCTGGGACT ATAGGTGCAT GCCACCACAC CCAGTTGATT
56051 TCTTAATTTT TTTTTTTTTT TTTTTTTGAG ACGGAGTTTC ACTCTTGTG
56101 CCCAGGCTGG AGTGCACTGG TGCGATCTCA GCTCACTGTA ACCTCCTCCT
56151 CCTGGGTTCA AGCAATTCTC CTGCCTCAGC CTCCCTAGTA GCTGGGATTA
56201 CAGGCACCTG TAATCCACCA TGCCAGCTA ATTTTTTGTA TTTTATAGTAG
56251 AGACAAGGTT TTAATATGTT GGCCAGGCTG GTCTCGAACT CCTGACCTCA
56301 AGCAATCCAC CTGCCTCAAC CTCCCAAGAT TTCTTAATTT CTTAATTTTT
56351 TGTAGAGACA GAGTCTCCCT GTGTTGCCCA GGCTCGTCTC AAGCTCCTGG
56401 CCTCAAGTGA TCCTCCTGCC TCAGCCTCCT AAAGTGCTGG GATTTAGGCA
56451 TGAGCTACCT TGCCTGGCCT AGACTCTGAA CAGTTTTAGT GAGATACCAT
56501 AAGTTTATCC AAGTTTCTTC TGTGTTGTAG CATATATTCT TTTTACTGC
56551 CAACCAATAT TCCCCGGTAA GGATATGCTA CGTTTGTCTA TCCGTTTCATC
56601 CAGCTGATGG GCATTTGAAT TGTTTCCACT TTTTGACTAT TATGGATTAT
56651 GGTGCTGTGA ACCTTGGTTA CAGGTTTTTT GTGGATTCTT GTTTTCATTT
56701 CTCTTTTGTA TATACTGAGG AGCGGAATTG CTGGCTCATA TAGTCTGTGT
56751 TTAGCACTTT GAGGAATGTA CACGTCTTCA CATAGATGTA TGTTTTTTGT
56801 CTAGACCATA CCCTTTTGTG ACAGGTTGAA CATCCGTAAT CAAAAGCCA
56851 AAATGCTCCA AAATCTAAAC TTTTGTAGTG CCAGCATGAT GCCACAAGTG
56901 GAAAATTCTA CACGTAACCC CATATGACAG GTTATAAGCA AAATTCAATC
56951 ACTTTATTTT ATGCACAAAA TTATTTTAAA ATGTCATGAA ATTACCTTCA
57001 GGCCATGTAT ATAATGTACA CATGAAAAAT AAATGTTTAG ACTTGGGTCC
57051 CATCCCTGAG ATATCTGATT ATGTATATGC AAATATTCCA AAATCCAAAA
57101 CAATTTAAAA TCTGCCACGT TTCTGGTCCT AAGCATTTTG GATAAAGGAT
57151 ATTCAACCCG TATTATGTTT ATATGCCTCT TCAGTGCTGG TAGTTGTAGC
57201 TTCTGCTTCC TCATCCCCTC ATTTGAGCCG GGTGGCAGAG CAGGGCAGAC
57251 TGCTGCCTTG CTCAGACCTA ATCGTTCAGT TCTTTCATTG TACAAGTATT
57301 CATTGAGCAG CAAACATAAG CCAGTCTCTC TAAGTGCTGG GATGTATCAG
57351 TGAATAAAGA ATATATGCCT GCTTTCATGT GCTTCCATTT TTAAGGGGGG
57401 AGATGGCAAA TAAATGTAAA GTGATAAATA ACAAAGGTTT AGTGGGGCAT
57451 TCGTAGTTCA GCGGCAGAAA TTTCGTCTCC TACGCGGGAG ACTCGGGTTC

FIGURE 3A-25

57501 GACTTCGGCC ATGCAGTCCT TCCATGCAGG AAGGGCTACT ACGTTTCTAC
57551 CCAACAAAGT TATTATGGCT GGACGCAGTG GCTCACGCCT GTAATTCCAG
57601 CACTTTGGGA GGCCAAGGCG GGCGGATCAC CTGAGATCAG GAGTTTGAGA
57651 CCAGCCTGAC CAACATGGAG AAACCCTATC TCTATTGAAA ATACAAAATT
57701 AGCCAGGCGT GGTGGCGCAT GACTGTAATC CCAGCTACTC GGGAGGCTGA
57751 GGTGGGAGAA TTGCTTGAAC CCGGGAGGTG GAGGTTGCGG TGAGCTGAGA
57801 TCGCACCATT GCACTCCAGC CTGGGCAACA AGAGTAAAGC TCTGTCTCAA
57851 AAAAATAAAT AAATAAAAAA TAAAGGTTCA TGTAAGTTTT GGGTGGCGAT
57901 GAGGGCGTTG AAGCAGTTAT GACCATGTAG CTACCATGAC TTTGAGATGC
57951 AGTCTTCTCG CAGTGTGCAC AGGCAGCATG GAGGGAGGCA GGGTACCGGC
58001 TCTCCCTCCT GAACCAGACG AGCTGTTGTG TTGCCAATGG AGGTTCAGGG
58051 AGCCAGTGAT GGGACAGCTC TGCTCCTGAG CTTTGCCACC CACAGGACCT
58101 GGGCACTGGA CCTTATGATG TGCTTCTCTG GAGTGAAGAC TGGCTGTCAC
58151 CTCAGCCCCC TCTCCTTTCT TCTGCTGCCA TATCATTCTT CACATGCCTA
58201 CCAGCCCCCT GGAATCTGCC CCTGCACCCT CATCCCTTAT ATATTTTGCA
58251 GAGAGCGTTT AGAGGACTGG AAGTGTGGCA TGTAATGGTA TCTCTGTTTC
58301 CACCCCGCAG CCCACCTTGG GACACCTTGA CTCCAAGCCC AGCAGTAAGT
58351 CCAACATGAT TCGGGGCCGC AATCAGCCA CCTCTGCTGA TGAGCAGCCC
58401 CACATTGGAA ACTACCGGCT CCTCAAGACC ATTGGCAAGG GTAATTTTGC
58451 CAAGGTGAAG TTGGCCCGAC ACATCCTGAC TGGGAAAGAG GTGAGCACTG
58501 GGA CTGGGGA CATGGCAGCA CCTCCCAGCC CTGTTGACAC TCCAGCAGGT
58551 GGTGATGGGA CTACTACTGC AGCCAACCTC TTGTTTATCC GGCAGAAATG
58601 AGATCTGAGA TATAGGGGTG CAAAAAGCTG TGGGATGAAA AGGAGTAAGA
58651 AATATAAAGG AGGAAGTAGA TTGGAATCCT GGGTTTCGCT GGTGAGAGAA
58701 GTGATTTGGG GCCTTTTGT CTCATCCTCA GGTAGCTGTG AAGATCATTG
58751 ACAAGACTCA ACTGAACTCC TCCAGCCTCC AGAAAGTAAG CACATGGCAC
58801 CTCCTGTCCC TTTTTTTTTT TTTTTTTTTT TTTTTTTGAG TCAGAGCCTC
58851 ACTCTTGTCG CCCAGGCTGG AGTGCAATGG TGTGATCTCG GCTCACTGCA
58901 ACCTCCGCCT TTTGGTTTCA AGCGATTCTC CCGCCTCAGC CTCCCCGAGTA
58951 GCTGGGATTA TAGGCACCCG CCACCACACC TGGCTAAGTT TTGTATTTTT
59001 AGTAGAGATG GGGTTTCACC ATGGTAGCCA GGCTGGTCTC GAACTCCTGA
59051 CCTCAAGTGA TCCGCTCGCC TCGGCCTCCC AAAGTGCTAG GATTATAGGC
59101 GTGAACCACT GCCCCAGCC CACCTGTCCC TTTCTAAATC TCTCTTCTGG
59151 GGTCAATGAT CTACTGACCC CATTTAGACC TTCTCTTGAA TTCCTAGTTT
59201 AAATTTTCTG GCCATTTTCG TCACCGTCCC CCAACCATTC CCTCCCATGG
59251 CTCTGCTACC TTCGGGGCTT TGGTTGGATC ATCTGTGGTG ACTCCTCCTG
59301 AGTGGGCTTC CTGGCCATAG GCACTGGCTC TTGTGAAGTC TTTCTGTTCA
59351 TTCCCAGCCA CTTGGCCTAC CTGTCTGACC TACTTCCTGC ATCTTGTTAT
59401 CTTCTGGCTT GTGGCCAGCC CTATGCAAAA ACACATGTTT GTAGCCACTA
59451 CTAGAAACAC GTGCAGCTAC TTCAAGATCT GGAATGATAC AGGGGAGTGG
59501 CTTTAGAAAT ACAAGAATAA GAGGAAGCAG GGAACCTGCC GGTGGGTTCT
59551 GTGCCAGCTA CCTTTTAGAG AATGAGCTCC AGCTCAAATT TTCTGAACAA
59601 AACCTAGTTC TGTTTCATCT GTGGCAAATC AGATATTTTC TCCATAAGCA
59651 TATTGTGGCA GTTGAGTTAG GAGAAGGCAT GATTCGTGCT AACAGAGTCA
59701 GATAGTGATA CTGGGAACCT TAGGAGTAAG GGCTGAGGAT TGTTGTTGAG
59751 GGCGATGCTC ATGGAATTAG AGTGGATGAG TTGTTCTCCG GACATGCAAA

FIGURE 3A-26

59801 TAGCCAGAAC CAAGGTGTTT CCTATTTATT GTTACCCCTG GGATCCCTTC
59851 AAGGGTTCTT CAGTTCAGTA GAAACATTGT TGTCATCATC AGGGTGTCTC
59901 TGCTTGAAGC TTTCCAGGAG GAAGGGAAAA AGGGCTGCTT ATGACATCCT
59951 GGCTCCAGCC CCACAGAAGA AGTCAGCGTG GGGTAGGCCA TTTGGCCTTG
60001 GGAGCAGTCT AGCCTGCCAT CGTAATAATC GCCAGTCCAC CAAGCCATCT
60051 TATTCCTGAC CTTGTTTTTC TCCCTAATTC TTCTTGGTTT TCTCCCTAAT
60101 TCTTCCTGAC TCTCTGGAAG GCACCAACAC CAGACAAATA GAGCCATTTT
60151 CAAAACCTTT TGAGACTCTT TGTTACTAAA GCCAGTCTGA TTCTGGCCAA
60201 AAATGTGATC TCAGCAATGA TCCCTGAAAA ATGAACATTG AAGAAGCTAG
60251 CCCCCTCAGG GGTCTAGACA AGCCCAGAAA ACCCCAAGTT CTCCCAGAAG
60301 AATGTCACCT CCATGCCAGG TGAGCAGCCT CAGGGGAAGA AGCCCTGGCA
60351 GCTGCCTCTG GCCCTATTTC AGAGCTGCTC CCCATTACTG CCCAGAGGGG
60401 TGGTATCCAG GCTTTTTGCC TCTCCATCCA AAATATCTGT TGGACCAGGG
60451 AAAAAAGTAA GAAAAACCTA GGCCCTAATA AAGGGTAAGG TCAGCATTGG
60501 GTTCCTGAGG ATTGGAAAGC CTTTTTCTTC TTTTCTTTTC TAGCTTAGGA
60551 AAGCTCTGGG GCATCATTAAG AGGGGAAACA AATGTATTCA CTTTATTCCA
60601 TAAACCATAT CTTGAATTAG GGCTTCCCCT ACCCCCAACA AAAACAACAA
60651 CAAAACTAG TTCTGTTCTT TGTGCAAGTG ATGAGGCCTG AAATTACAAA
60701 AAGCCCCACC TCCAGTTCTC TGGCCCCCGC AGAGGGGAAG GAGTTCATTT
60751 CTGTCATCTT TCTTTATGGA AATACATGGT TTGGAGCCCC TGGTTTTGTT
60801 TCACAAAGAG AGCGTGAGTG TGTGGAGGTG GATTTGATTA AAATTGGCAT
60851 CAGCTATATA TAGGAGTGGC TTCTTCTGTC ACCACCCTAG AGGCCAGGA
60901 AGGAAAGGCC TATCCCCTAG AACAGAGCCC TCTGACTACT GTAAATCAGA
60951 AAATGATGGG GTCCCCCTCT GGTGCTCTAC CACCCCTTTA CACAGACCAA
61001 GCTGGGGTGT GTACTGTCAC TGAACCAAGG CAGCAGCTCG GATTCTGAAT
61051 ATTCACGCAC ACGGGCTCAC ACTCCCTCCA GTAGAGGCAC CCAGCCAAAA
61101 CCTGCCTGCT GTTTTGGGGC TGGATTTGGT AGACGCAGCA GAGGGCATGG
61151 CTGGCTCATC CTGATGCCAT CCCGGGTAGC ACGTCCCCAC AGCCAGCCCT
61201 CCTCCAGCTT CCCCAACTTC CCAGCCACAG GGAAGGCCGT GCATGAGCTA
61251 GACAACCACC CTATTTTCTT TTCCCTGCCC GGTTTTGGTT TTTTGGGAAA
61301 AACAAATCCT GGCAGGGACT GTTTGGAGAG ACCTGATGGG AGCAAGTTGG
61351 GCAGGCATGA CCCCTGGTAT TTTATCTTCC AGCTATTCCG CGAAGTAAGA
61401 ATAATGAAGG TTTTGAATCA TCCCAACATA GGTGAGCACA AGTTGTTATT
61451 TCTTTCTTCT TCCCCAACAG CAAGGCACTG CTTTCCAGCA TGTCATCTTC
61501 TCCCCGAGGT GCACTGCCTT CTGGAGTCTG CAGTCTTCAA GGATACCCCT
61551 GGGGAAGCTC AGCTCAAAAT CCATCTCCCC TTCTGGCACA CTGGGCTGTC
61601 TTTAGCAGTT TGGCTGGCAT GAGAGGAACT TGTTCTTGGG AGTGGGGGAT
61651 CATGAAAGGA GGGGAGACTT TCGTTCCTAG GATGCTCCTG GACATGTTGG
61701 AGAGCAGTAT GTGGCCCTG TTGCTTCTTG ACTTAAGGCT TGGCCTTTTC
61751 TCTTGTAGTT AAATTATTTG AAGTGATTGA GACTGAGAAA ACGCTCTACC
61801 TTGTCATGGA GTACGCTAGT GGCGGTAGGT GTGGAAGTGC CTCTTCCTGT
61851 TGTGCCCCCA CTTCTTCCAC CTCCAGCCAG CTCTGACTGA GATCCCTGCC
61901 TGGTCTCTTA CAGGAGAGGT ATTTGATTAC CTAGTGGCTC ATGGCAGGAT
61951 GAAAGAAAAA GAGGCTCGAG CCAAATTCCG CCAGGTAGGT GTGACTCCCT
62001 CCATAGGAGC TAGGCCTGAC CTCTGCTTTT GGGGTTTGAC ATGTAAGGAT
62051 AAGCTGCCTG TCTGTAAGTG GCCCTTGGAG GGTACTTTGG GCTCTGCTTA

FIGURE 3A-27

62101 TCCGTGTGGC AGGTTAGCAC TAAGTCACAG GGTCAGTCT CTGTCAGCCC
62151 CTGTGGCCCA CCCTCAGGCA CCCCTGGGTT AACCCCTTCTT CCTTCCTTTC
62201 AGATAGTGTC TGCTGTGCAG TACTGTCACC AGAAGTTTAT TGTCCATAGA
62251 GACTTAAAGG TAAGGCATGC ACTTCTCCTT GTGCCTTTGA GTGGGAGCCA
62301 GGTTGTTGCC TCTTGTTTCT CCATGATAAA ACCATCAATA ACCATCAGGC
62351 CCTGAGTGTT CCAGGAACT CCAGCCTTTC TTTTTTCTT TCTTCTTTC
62401 TTTTTTTTTT TTTGAGATGA CCAGAAAGCC CCTAGGGCTG CCTCTGATAG
62451 AGGCCTTGTG GCTGGACCTC GGGTTCCATT CTAGCCCTTG AGCAGGGGCC
62501 CTCTGCCATT TCACCTCTTG GCACATCACC TTTTAGTGCT GCCAAGCAAG
62551 GCAGGCACAC TCCAGGCTTT CTCAGTCTTT CAGGCAACCT GGTAGCTGAC
62601 CCAGGGAAGA GTGCTGAAAG TTCCACAGCT GTATCCCAGC TGCTTTGCAG
62651 GCAGGCACAC ACATACCATC TCCATCACC AGATACTCAA GTTTGAGGAC
62701 ACCTGTGGGT CTCTTGCTG CTGAGTCCTC ACAGACATGA TTTGATTAAAC
62751 CTGGGCCTGA TGCTGAAGCT TTGCACAGCT CACAGGGTCT CTGGGCCTTC
62801 AGATCCCATC TCTCCCATGG CTGCCCACGT GAGGAGTGGC CTGCATTGCC
62851 TTCCTCCTGC CCAGCCTATT CACGCTGATT GAAGCCCTGC CCTGAAATTG
62901 GTGGAGAAAG TTCTGAGACT GAAGATGACT TTCCGTTTGT TCTCCCATTC
62951 CCCTCAGTCT CTCTCTGCCC AGGGCCTTAG TCTGGTCCAC TTGGTTCCCT
63001 GATGTTTTCC ATCTTACCTC CCAGGCAGAA AACCTGCTCT TGGATGCTGA
63051 TATGAACATC AAGATTGCAG ACTTTGGCTT CAGCAATGAA TTCACCTTTG
63101 GGAACAAGCT GGACACCTTC TGTGGCAGTC CCCCTTATGC TGCCCCAGAA
63151 CTCTTCCAGG GCAAAAAATA TGATGGACCC GAGGTGGATG TGTGGAGCCT
63201 AGGAGTTATC CTCTATACAC TGGTCAGCGG ATCCCTGCCT TTTGATGGAC
63251 AGAACCTCAA GGTGGAGTGA AGTGCAAGCT TTTTATTGCT TCTCATTTCC
63301 TCTCGGCCTC TGGTCTTAGC CCTGACCTCC TGCCTTTGCC ACCTGTCTAC
63351 ATTTGTCCCA AGCCAAAGCT TCAGAGAAGG GCTTGCTGAG GTAGCAGCAG
63401 TCAAAGGCCT TCTGCACCTG GGAATGAATA ACCTCAGTTC CTTTCTCGAA
63451 AGATGGGATA AACTGTGTGT GTGTTTATCC CCCAAGGCAC TCCGGATTGC
63501 AGGCCTCGGA CTGGTCAAGT TAGAGGGTAC GAGGGTATTT GACTTCACTT
63551 GCCTCTCTGG TGAGGTGTCT TGTCCCCAGG CTGTCTGCCT TCTTCCATAT
63601 TTCATTTATG TCTGCTTTGC CAGGCTTAAG CTCTCAGGAT CTTGGATATT
63651 AGGTTTCTTC CTTTGGCCTT GGGGTGATTT CAATTTTCTA ACCCTGGATC
63701 CTCCTGCAGG AGCTGCGGGA ACGGGTACTG AGGGGAAAT ACCGTATTCC
63751 ATTCTACATG TCCACGGA CTGAAAACCT GCTTAAGAAA TTTCTCATTC
63801 TTAATCCAG CAAGAGAGGC ACTTTAGAGG TGAGCAGTGG AGCCCAACTG
63851 GCGGAAGGGC CTGGGGTCCC CACAGAACT TTCCAGCTGA GTTTCTTCCC
63901 CCTGCCCTTT TCCTTCTCTG TGCTCCCCAG CAAATCATGA AAGATCGATG
63951 GATGAATGTG GGTCACGAAG ATGATGAACT AAAGCCTTAC GTGGAGCCAC
64001 TCCCTGACTA CAAGGACCCC CGGCGGACAG GTGAGGCTGT GCCGGGCTGT
64051 GAGGTTAAGC TTGCCTAGGA GTTGAGGCCA GTCTTAACTG TATGTCCCCC
64101 TGTGCAGAGC TGATGGTGTC CATGGGTTAT ACACGGGAAG AGATCCAGGA
64151 CTCGCTGGTG GGCCAGAGAT ACAACGAGGT GATGGCCACC TATCTGCTCC
64201 TGGGCTACAA GAGCTCCGAG GTGTGTGCTC CCCGCTCCAT TCTCTGACCT
64251 GGCCAGCCTC ACTGTCTGTA GCACCTATGC TTCTAACACC TGTTGAGGGC
64301 AGAAGCTCAT CTCTGAGTAG GTGTGCTCTC TGCTACCAA TTTTAAGCCT
64351 CAGCTTTGGT GTCTAAGGTC CTCTGGCCA TTTACTGATC TCCATGAGTG

FIGURE 3A-28

64401 AATTAATAGA AAGCTGGTAG GGTCCGTGTG GGA CTGGGTC AGAGTTTCAA
64451 TACGGGTGAG TTGATCTAGG TTAGTCTGCA TTGATTAGAT GTGTCTAGGT
64501 CATCGGCTAG CACTACTACA TTGATCTAGA TATCTTTGTG TCTCTTTTGT
64551 TATCTGGAAG TGTACATTTT TGGGTGTGTG TGTGTGTCTC TGTGTGTGTC
64601 TGATCGGAAG TTTGAGTCTG TTGCTTTTTT TTTTTTTTTT TTTTTTTTTT
64651 GAGACGGAAT TTCGCTCTTG TTGCCCAGGC TGGAGTGCAA TGGCAGGATC
64701 TTGGCTCACT GCAACCTCCG CCTCCCGGGT TCAAGCGATT CTCCTGCCTC
64751 AGCCTCCCAA GTAGCTGGGA TTACAGGCAT GTGCCACCAT ACCCGGCTAT
64801 TGAGTCTGTT GCTTCTGTCT AGTGCTTTAT GTTTGGGTGT GTGTATCTGT
64851 GTGTGTGTGT GTGTGTGTGT GTGTGTGTAT GTGTCCGTCT TCCCGTCTGT
64901 GGATCTGGAG ACTTTGTGAT TGTTCTTCTG CCCATTTGGG TTTTGTTCAT
64951 CATCTGAGTA TCCCCACATG AACTCCCAGC CTCCCTGCCC TGCTCTCCCT
65001 CTGGTGGTGG GATCCTTAAG AGGCACCTGG TGACACTTGG TATAGGCCCA
65051 TATTGCTCTG TGTTGAGGGG AGTGGACTTG AGTCTGGACA TGTGTTCTTG
65101 CGGATGTTTG TGTCTCTGGG TGTGTGGGCT TATGTATTCC TTTCTGAGAC
65151 TGTGTTTGTC AGTGTCTGTG TCAGAGCATG TGTGTCTCCA GGGTCTCCTC
65201 CAGGGGGGAT GTATTGGTCT TACAAGTGGA TGTCCGGTAT GATCCTGGGG
65251 TGTTTGAGTG TTGGGAGAGG GCGGTATGTG TAAATGTGTC CATCCATAGG
65301 GATCTCCACA TGACTTCTGC CCTCCCTTGA AGCTGTTTTC TGTTCCTTTC
65351 AGCTGGAAGG CGACACCATC ACCCTGAAAC CCCGGCCTTC AGCTGATCTG
65401 ACCAATAGCA GCGCCCCATC CCCATCCCAC AAGGTACAGC GCAGCGTGTG
65451 GGCCAATCCC AAGCAGCGGC GCTTCAGCGA CCAGGGTAAA TGCTTTTGGG
65501 AGTTGTAGGT GGGGACTCAC CCCTCTCCAG AGAGGTTACA GTTCTGTGG
65551 GGACTTGGGT AACACAATA AGTTTCAGTC CTGGTTCAGC CACTTATTAG
65601 TAGTGTGGCT ATGGGCAAGC CACTTCCCTT CCCTCGCCTC TGTGGAATGG
65651 GGGCTTGCTG GGTTGTTGGC CAGCCCTGTA GGAAATGAGC ATGCGTGGGG
65701 CTGGCACTCA GTGGACCCCT TGGCCTTACC CATTCCCAC CTCCCTCTGG
65751 CCCAGCAGCT GGTCTGCCA TTCCACCTC TAATTCTTAC TCTAAGAAGA
65801 CTCAGAGTAA CAACGCAGAA AATAAGCGGC CTGAGGAGGA CCGGGAGTCA
65851 GGGCGGAAAG CCAGCAGCAC AGCCAAGGTG CCTGCCAGCC CCCTGCCCCG
65901 TCTGGAGAGG AAGAAGACCA CCCCAACCCC CTCCACGGTG AGCCGCACCC
65951 CCCGCTCTCT CCTTCCTTCC TGCGGTGGGG CCTGCCCTCT CCAGGCAGCT
66001 CTTCTCTTAA TTCAGACTCT GTTCCCTTTG GCTACTACTT CTGCTTATAG
66051 CAGGAAGCCT CGCTCCCAGC AGTAAATGCA GAATCCTTTC CTTAACCTAC
66101 CACTGTCTGC TTCAGGTGGA AGGGACAGGA AGCCTGTTCC ATGAACCTGG
66151 GGGGAGAACC TGGCTGTAGA CCACTTTGGC TTTCTGATAG AACGCTTGCC
66201 CTTTATTCCC CACAGAACAG CGTCCTCTCC ACCAGCACA ATCGAAGCAG
66251 GAATTCCCCA CTTTTGGAGC GGGCCAGCCT CGGCCAGGCC TCCATCCAGA
66301 ATGGCAAAGA CAGGTGAGAG ACCCGGGCCC TGCCTGCCTC ACTCCCTAGG
66351 AGCCATGTCT CACAGGGTGA TGTCTGTCAG CAGCACCGTC TCCTGTCCCT
66401 GCCAGCGCAT TGCTCCCTGC TCCCTGGAGT TCCATCCTGG CTGTGTCCAG
66451 TCCAGCTTTC CCCTCCCCTA TTCCACGCCA TTGCCTCCTC CCCATCTTCC
66501 TCTGACTGCT ACTTGAGT TGGCAAGTGT GGGGCTGACC GTGGCCATCT
66551 CAGCTACATG CTCGCTTCTT GACCACGGCC AGGGCATGGC AGCTGCCCTC
66601 CTCTAGACAT GAGCAGCTAA GGCCTTGTGT TGGGGGTCCC AGCTCAGGGC
66651 AGAACCAAGA GATGCCACC TTGAGGGGTG TACACATAGA GGGCGACTCC

FIGURE 3A-29

66701 AGCCATCCCC ATGAGACCAG AGCTCCCCAG CCTTCACCGG CCGCATTTCT
 66751 TGGTGTGCA TTCCTGGCTC TATCTCTTCT GAGTTTATGA AAGTTTCCCC
 66801 TCAGCAACAC CCCACTCTTT CTGTAGAAGA AACTCTCCTG TTCTTAAAT
 66851 TCTTAGGAGG CCAGTGCAGC CTGGAGGCAG CGGCCCTTG TCTGCTCTCC
 66901 TTCATTTCTG ATTCTCTTTC CCAGGCACTG ACCCACCTCG CTGCTTCCCCG
 66951 ACCTCACTCA CCTCCACTTC TCAGCCCCGC ATTCTCAGT TCTGACTTGC
 67001 ATCCCCGCTG TGCCAGGCC TGACTTCTAC CCTGCCAGAG CTCCCCAGCT
 67051 CTGGCCCTTC CCCTGCCCTT GCTTCCTAAT CCAGGCCTCC CGCCCTCACT
 67101 CACCCCTAAC ACGGGCCTCT CCGCTGCTTT TGTTTCCTAG CCTAACCATG
 67151 CCAGGGTCCC GGGCCTCCAC GGCTTCTGCT TCTGCCGAG TCTCTGCGGC
 67201 CCGGCCCCGC CAGCACCAGA AATCCATGTC GGCCTCCGTG CACCCCAACA
 67251 AGGCCTCTGG GCTGCCCCC ACGGAGAGTA ACTGTGAGGT GCCGCGGGCC
 67301 AGGCAAGTGT GCTGGGGCAG CTGGTGCACC TGCTGCCCTC AGCCACCCCT
 67351 ACCCCCTTGC CCAACAATT TCTTCTTCCC ACTTGGGGGT CTGCTGTGT
 67401 TCTTGTGATC TTAGCCACAA GAAATGGGTC TGTCCCTGC GGCCAGGAAG
 67451 TGGAGGGAAC AAAAAAGAGC ATTAATGCCC CTCTTTTCCA GTTCTCCCTC
 67501 TCAGAACAGG TATGCAGGAA GCTGTCCTAA GGCTCCAAAG GGAAACCTTT
 67551 TTGTTCTGAA CTTCCAGGG TTTCCTTAGG GACCCCGGGG ATAGTCGGCA
 67601 TCACAGGGAC TCAATCCTCA AGGGTTGGTC CCCATTGCCG CTTGAGGGT
 67651 CCAGTCTGCC CGGCTCCCAG GGAGCCCGCT GTCTCCAGCC TAAACCACAC
 67701 TCCACACAGG GGTCTTCTC TGCCTCCCTC CCTCCCTTCC CAAACCATCT
 67751 CTTTCCACTT CCACGAGACT TCCTTCTCAC CACTGTCCTC AGTAGTCACA
 67801 CCCTTCCTTC TGTGTCCTCG TGATGGCTGC CTCTGCCCTA GCATCCCCCT
 67851 CCCTGTCCCC ACCACAGGGT GTCCAGGTGC CCAGTGATGG CTGTCTGTGA
 67901 CCCTAATTG TCCCCCTCAA CCCACTTCT CTTCCACAG CACAGCCCCC
 67951 CAGCGTGTCC CTGTTGCCCTC CCCATCCGCC CACAACATCA GCAGCAGTGG
 68001 TGGAGCCCCA GACCGAACTA ACTTCCCCCG GGGTGTGTCC AGCCGAAGCA
 68051 CTTTCCATGC TGGGCAGCTC CGACAGGTGC GGGACCAGCA GAATTTGCCC
 68101 TACGGTGTGA CCCCAGCCTC TCCCTCTGGC CACAGCCAGG GCCGGCGGGG
 68151 GGCCTCTGGG AGCATCTTCA GCAAGTTCAC CTCCAAGTTT GTACGCAGGT
 68201 AAGCAAGGAG CTTTGGGTGG CAGAGAGGCT CAGGCCAGGC CTTCTGTCTT
 68251 TACTCGGGGT GGGTTGGGGT TTGGGGGTTG GGGTTTGGGA CACTCTGTAC
 68301 CGGTATTGGG TCCTGGGGTT AGAAGAGGCT TCAGGAAGCA CAAGAAATTA
 68351 GGTCTTTGTC AACACCTTAT GTGCCCAGGC CCACCCCTCT TAGGCCTCTC
 68401 CCAACTCCT CACAGGCACC CCTCATTCTC TGGCCCCAAG CAGATGGCCG
 68451 ATGCCGCCTC CTCTCTAGGA GAGTGTGAAC TCAGATGCTA AAATAAAAGC
 68501 CCCCCCTTCT CTCCTGGGTT CCCATGGAAA CTTATATTTG GTGACGCAGC
 68551 TGCAAAGTCA TGAGGCATGA GCCAGGCTGG GGCCAGCAAG GAAAATTTTG
 68601 TCCTGGTCTC TTGCCCCCTT GACTGCCTCT CCCACTAGTT GGTCTGTCTT
 68651 CTGGCTGCAG GCGCAGCCAT GCCCTTCTGC CCGGGGGTTT TAGGGTGAAA
 68701 CCTATAAATG AAATCACTGG CGAGGGCCTA CAGTGGCCTC TTCCCTAACC
 68751 TAACTCCGAT GTGCCAAAGG TTTCTGTGT TGGACCCAGG GTGGGGATCT
 68801 CTTACGGGG TTTCTCACAC CTGAGCCCC AGCCACCACA GAGGTGCAGC
 68851 TTGAAGTGCA TCCAGCCAAC TGGCTGGCCT CCTGGGATGC TCCGCATCCC
 68901 CATCCTGCCA TTCCTCTCCC TGCCTTGGAG TAGCAGCTCA GGAAGCAGCA
 68951 GGGGCTTTGA GAGAACAGGC TCGCCTGCC TTCTCTACG TTTCACTCCA

FIGURE 3A-30

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69001 CTCTGCTGGA GGAGCCAAAG CCACTGCCCC ATCCGAGCCC CAGAATGCAA
69051 GTGTGAGGCC TGCAGAGAGT GTGGGCAGGT CTGAAAGCCT GGGACTCTAG
69101 TCTCGCTGAG CGGCTCTTCC GAAAATGGGA TGACCCTTGA ACCTGTAAAG
69151 CCACCTCCCC CACCTGCTTA TCCACATACC GTCTTGTTGG TTTTTTTTTT
69201 ATTTCTTTTT TTATTTTGTG TTTTTTTTGT TTGTTTTTTT AGAAATCTGT
69251 CTTTCAGGTT TGCCAGAAGG TAGGCGTTGA GCCCGCTGTG TGTGTGTGTG
69301 TGTGTGTGTG TGTCTGTGTC CTGTGTCCTG CCTCCATCAC TAACTCCCCT
69351 TTTCTGGCTC TTA CTCTCCT CCATCTGCTT AACCAAGTCT GTGTGGCCCT
69401 CCTCTCTCTG CCATCTTAAA GGGATGAAGA CTGCCTCTGA TTGGGCATCA
69451 GCACAAGGCC TGCCCTCCGT GCCCCCAGTA CAAACAGGCA GGGCTAAGAG
69501 GCCACATTGG CCCACTCAGG GCAAATGGCT TTAAAAATGA GGGCCTTCCT
69551 TGGGCCCACA GTTAACGCCT GTCCTCAAGT AAGGGGAGAC TGTCTCAGGG
69601 AAGCCTCCCT TTAAGATTGT CTCCTCTCAC CCACCCACC CCACCCACC
69651 TCCCTCTCAC CCCAGGTTTT GGTCAAGAAG GTTGGGATCC TTTCTGCCC
69701 TTTCCCTTGT CATGTGCATG CGCTATGAGG AAGCTCCAGG GTTACAAGTG
69751 CATCTGGGAT GGTATCTTGT TTGTTGTCTC CTGGGTTTCC TGAACCTCAG
69801 AGCTATGTGA CCTCTTCCCC GTGGCCTATG GGATCGCAGG ACTTTGGAGA
69851 CACTACGGGG ACCCTGGGGC CCCAAGGTTT CAGTCTGGCT CCCCAGACC
69901 TTAGGAGCTT TTGTCTCACA AATGGAGCAC AGCACCCCT CCTGGCAGCT
69951 CCTGCAGAAC TAGCCCCACC CACCCGCACC CCTGCCCCAG CACCCCTGCC
70001 ACCAGCAGCA TCTGGATAAA TCAAGCCTCT TCTCCTCTAG GCTGTTTTCT
70051 CCAGATATGG CCTGTCTCTT CCAAAGTGCG GGGAGCTGGG ACATTCTAGG
70101 GCAACGGCCA TTCTACCCCA AGCCGTAGCA AAACAACAGG AGATCTCTGC
70151 ACCCTTACTC AGGGGTCTCC CTTACAGTC CCCTTCCTGG CTCTTTCACC
70201 CCTGGCCTTA TGCTCATCCT CTCTGCAGGC CTCGGGGACC AAATACCAAG
70251 CTGAAGACCA AGGGCCAGGT TAAGAGTGCT TGTTCCCCAA GGCTGTCTGC
70301 TCAGGCCCTG CATTGGGACT GGGATGCCTG GCAGGCACAT TGGTGCCACA
70351 GCTGATGGAG GAACGTCCAG ACAGGTCTT CAGGCTTTCC CTATCCCCTC
70401 CTCCTCCCAC CCAGCTGTTG ACTGCATGAC TGGCTGCTGC CTCAAGGGGC
70451 CCCAGCAGGG GGCTGCCCCA CAGGGGTCTT GGAGAGAGCA GGGAGGGTGC
70501 CTTCTCGCA CAGCCGGGCT CCCTGCTCGC AGTGCGCTTG TGTGCACCCC
70551 TGTGTTGGTT GTGTCTTCCT GTTTATTTCT ATGTGCTGCT GCTCTTCCTC
70601 CTTCTCTCA CATCCTTCCT CCTCTGCAAT CCCCAGTTT CTAGCTCCAG
70651 ACACCCATCT TCCAGCCAGG AGCTGGAGAA GCCGCTCAGC GGGGCCAGAC
70701 CTCTTCCCCA CCCACCCAAC CAAGGTGTCT GCCCTGCCCT GCCCCACCCC
70751 ACCCTCATCC TCCCTGCGTA TGAGCAGATG GCCTGGCAGG CCAGCAGGTA
70801 GGGGAGTTGG GAAAGGTCGG AGGAGGCCGC CTTTTCCACT CAGCAGCAGG
70851 AAGCCATCCC CAGGTGCCTA CCATGCAGAC CCAGGCCTTG GCACTTTGAG
70901 TCTCTGACA GGCCCTTGCG TAGCCACGGC CCCTCCTCCT ACAGAGATTG
70951 AAAGCATTGC AGCCCTTTT CTCCAAAAGG ACTGCAGTCC TGAGACCCTA
71001 GCGTGTGGCT CAAAAACGC ACTCACACCT GCAACCCCCA GAACAGCGCG
71051 TGAGCCCTGG CTGTGGGGGA GCAGCCTCGT GCCGGGCCGT GTGCTCAGTG
71101 TGCTCAGTGA AGTGCGTGCA CAGCCACTCC CCCTCCTCCC CCAGAGCAGA
71151 GGCTCCTTCT CCCCGGCACA GATCTGGGAA TGTGGGGAGG GACAAGCCCC
71201 ATGTGCTGGG CTCCCTGCTG GAAAGGAATG GTTGAGCCGC CAGTGTGAGG
71251 TGCTGCAGAG CCCTGTTGGC TTGCCAGGTG ATGGGCAGAG GGCCCTGGGC

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FIGURE 3A-31

71301 TTGGGTCCTG CCCACCCACT GGTGGCACCT CCCCAGACCC ACTCTCATCT
71351 GGGTCTGTGG CGGCGGAAGG AGCGAGAGAT CCCAGCACTA AACTCTCCCT
71401 CGCTCTGTTT TTTGAGGAAC CTGAATGAAC CTGAAAGCAA AGACCGAGTG
71451 GAGACGCTCA GGTGAGAGGG CTGGAGCCAG CACTGGCCCT GCCCGGGCCA
71501 CCGGGCTTGC CACAGCCTCC TGCTCCTCTC TTCCTTCTGC CACTTGGCTC
71551 TTCCTCCCGT GGTCTGCCC TGTCCTACC CTCTGGGGCC TCCCTTTCCT
71601 CAGAGAGTTT CCCCTTCCCA AACCCAATTG CAGGAGTTAC GGGCCCTTCT
71651 CCTCAGGTCT GGTATATTCT GGAAGTCGGA GTTCTGGGTC GGGTGGTTGG
71701 GGCTACAGAT TCCTACCCCT GGAATATCCC ACCTCCCTGT GCTCGGAGGC
71751 TGCTTTCTGG AGAGAGAGTC TGTGCTCGTG CTGTTGAGGG CACTGGTGTC
71801 TTCCCTGACC CCACCCCGCC TACCCCAAGG CTGGCTTCTC CTCCCCTTCG
71851 CTGCTCTGAG AGATGGGGGT TGGAGGACTG CCACCCTCCG CCCCCGCAGG
71901 CCAGGGGGCA CGCCTGGCTG CTCCTGCTCC CTCCCGCTCT CCTCTCTGGG
71951 CTCAGGGGCT GTCTGCCAGG GTGGCTCTCC TGGGGTGGGG TGCCTCAGCC
72001 CCCCCGTGAC GCCCGCCTCT GCCCTCTCCA CAGACCTCAC GTGGTGGGCA
72051 GTGGCGGCAA CGACAAAGAA AAGGAAGAAT TTCGGGAGGC CAAGCCCCGC
72101 TCCCTCCGCT TCACGTGGAG TATGAAGACC ACGAGCTCCA TGGAGCCCAA
72151 CGAGATGATG CGGGAGATCC GCAAGGTGCT GGACGCGAAC AGCTGCCAGA
72201 GCGAGCTGCA TGAGAAGTAC ATGCTGCTGT GCATGCACGG CACGCCGGGC
72251 CACGAGGACT TCGTGCACTG GGAGATGGAG GTGTGCAAAC TGCCGCGGCT
72301 CTCTCTCAAC GGGGTTCGAT TTAAGCGGAT ATCGGGCACC TCCATGGCCT
72351 TCAAAAACAT TGCCTCCAAA ATAGCCAACG AGCTGAAGCT TTAACAGGCT
72401 GCCAGGAGCG GGGGCGGCGG GGGCGGGCCA GCTGGACGGG CTGCCGGCCG
72451 CTGCGCCGCC CCACCTGGGC GAGACTGCAG CGATGGATTG GTGTGTCTCC
72501 CCTGCTGGCA CTTCTCCCTT CCCTGGCCCT TCTCAGTTTT CTCTTACATG
72551 TTTGTGGGGG GTGGGAGATT GTTCTCCAGC ACCCCACATT CACCCCTGCC
72601 CAGAGATTCC CCCTTCTCCT CTCCCCTACT GGAGGCAAAG GAAGGGGAGG
72651 GTGGATGGGG GGGCAGGGCT CCCCCTCGGT ACTGCGGTTG CACAGAGTAT
72701 TTCGCCTAAA CCAAGAAATT TTTTATTACC AAAAAGAAAA AAGAAAAAAA
72751 AAATCCCAGC GGCCACCTTT CCTCCCTGCC CCATTGGGAC AGTCGAGACT
72801 GGATCTGTGG GGTTCCTCCG GAGGGTGGCT CAGGGCTGGA ACACTCTCAG
72851 GCAAGAGTGG TGGAGCTCCC GTCAGGCCCT CCGCCAGGCC CACTGTGGGC
72901 TTCTCCCCTC TCCTCCCTCC TTCCCCTCCA AGCAAACCAC CAGAGGTGGC
72951 CTTCCCCTGA CCTCAGGCCC CTGGGCTGGA GGCCTGGGCG GTGGGGCAGG
73001 GGGCGGGGGT GCTGCGCAGC CCTGCACTGG GTGGGGCTGG GGGCTGCTCC
73051 GGGGCTGCTG AGGCTGGAGG GCCGGCACAA GGCTCCGCTT CCCTCCACAC
73101 TGTACCCTCT GCCCTCCTC CCCAGAGCTG GGCATTTCTT TCCACAAGCT
73151 GCTGTGGGGA CGTGTGTTCC CTCAAAGTCT GTGCCATCTT CTCCCACCCC
73201 TCCCGGGTAG AAGGAGGGGC TGACCCAGG GCTGGGAGAG GGGAGGGGAC
73251 TGGAGGGCAG ACTGGCTTCT CGGTCCCCAG GGGGCCGCTT GGGCTGTTGG
73301 TCTCCAGAGC AGGGCCACTG GGCACCTCTG GATGGGGGAG CCTTTGTCTG
73351 AAAGCACAGC CCCCTCGCCC TTCCTCTCCC CATGGCTTCC CTTTATTGG
73401 CATTAACTG GGCACCAGCT CTCTCCATAG CAGTGACTTC CTCACCACT
73451 CTCATCTCTC AGCCTTGCTT TTTCTTCTG ACACTGTCGC CCCCTCCTCT
73501 CAGGAGACAC TGCCGAGGGC CACCTGGCAG AAGGCTGAGT TAGGCAGCAG
73551 GGCCGGGAGC GTCTGCCCTC CACAGGGTGG GGGACAGATA GGCTAAGCGA

FIGURE 3A-32


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73601 CTCCCAGCTT GCTACCCTCA GTGGCCAGTG TGGGCGTGGG CGGTTTGGGG
73651 CGCTTGGCTG GTGGTGGCCA CTGCATCCCT TAATTTATTT CTCTGCTGTT
73701 TCTGTTCTTG AGAAATTGGG GGTGGGAGTC CTACACAGAG GCTGCCCCTA
73751 CCCTCACCTG AGTTGTACAT TTTTTTGTGA TGGGTTTTAT TTTTATTAT
73801 TTTATTTTAT TTTTTTTTTT TTTTGATTTA TGATGACTCC ACCCCTCTTC
73851 ATCACCCCCG CTCCCAGGCC AGGCTCAGCG ATTAAGCCGA GCCCTTGCGT
73901 CCTAGGAAGG GGCCTTGCCA ACCTCAGCCC TCCTGCCCCA CACTCCTACT
73951 GCGGCTCAGA CCAAGGGCTC CCCCTCCCTC CCTTCCCCCC TCCTGCCCTA
74001 TGGAACAGCC CGGGTGCTCT GAGGGGGCTG GGAGGGCATG GCTTGGCTCC
74051 CAAAGGGGGT AGGGGCCCCG GGCACCCAGG CAAGGTGGCC CCTCCCCGTC
74101 TAGCCCCCTC CTCCCCAACC CTGCACTTAG TTTCTCCTCT GGATCAAACA
74151 CGTAATAAAG AGAATGTTTG GAATCTGAGC TGCCTCCTCC TGCTCTTCT
74201 CCCAGCCAGG CAGGGACCCA GTCTCCTGTG GGCAAGATGT GGCCTAGCCC
74251 ACCTGCCTTG CAGGAGAGAC TTGATTCTCT TCTGGGGCCA GTGCTGGGTG
74301 GGCCCAGCTC CCCACTTACC CACAGGGCAC AGACAGGAAG CAAAGCCCAG
74351 GGCCCTTGCA CCAAAAGGGA AAGAAAAC TC AGTAAGCTTA GATTTTATTT
74401 TTTTAAATTT TTAATAAATG TTGAAAAATA AATCCATGTC TGCATAAGTT
74451 CCCAACCCCC ATTTCTCCAA GTTCTGGAA GGTGGGCTTG GTGGGCACCC
74501 TCAGCTCCTT AGCATTTCCC AGCTGGCCCC TGAAGACAGA GCTTCTCTTC
74551 CAGCCTCTGC TGCTGTAAGG CCCCTCTGCC CACCTCCCCC CCTGCAGCCT
74601 CCCTCCCCAC CTCACCCAG ACTTATTGCT AAAAGAAGGG AAAGAGGAAT
74651 GAGAACAGCC AGCACACCCA ACTGCCCTCT CCCCCTCCA CGCTAAGGTC
74701 ACTACCCCGG ACACACAAAG GGCAGGACCC AGAGGCCAAG CCCCAGCAGA
74751 CTAGGACACA GCCATTCCAG TACCGGCCAG GAAGCGAAAG TGCCCTCAGG
74801 CCAGCTCAAA GGCCCTGAG CCCGGCCATG GCCCCAGGAG ACAGGCCAG
74851 CTGCCAGGAA CACATGCAGA ACCCAAAGGG CGGGGCTGGG CTGTCCGAAA
74901 CTCTGGTCTT ACAAAGACCC CGCCAGAGCC CTAGTCCCTT CTGTCTCAG
74951 TGACACCAGA GATGCCTGGG GATGGCCAGC AAAGGGGTCC TGGAGCCCGT
75001 GGTTGGTGGA GGACGTCAGG GCTCAGAGTG AGGGTGCTGG GGGCTCCAGA
75051 GGGGTTCCAA TCAGGGTGGG TGGGGGCTGA GGGCCAGGGC GGGCGCTGTG
75101 GCGGGGGGCA GCCAGAGCGG GCGGATGAG AGGCGGTGGG GGCTGGTTGG
75151 GGGCCAGCCG GGGCTGGAGG AAGCGGCCCT GCTGCAGTGG GGGTGGCTGT
75201 CGGAGCAGAG TGGGAGCCGT GGGCAAAGGT GGCCTCAGCA GCGGGGTGG
75251 CTGGGACAGC GAGGTGGGAG GTGGAGGGGG TGGTGGCGCA GGGGGCACTG
75301 ATCGGGGCAC GGACGTGGAG ACCGATGTAA TCTGGACCTG AGGGGAGAGG
75351 AAAGAGTGAG AAGCCAGGCT CTTCCCGCCC TCAGCCCAGT CTAAG (SEQ ID NO:3)

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FEATURES:

Genewise results:

Start: 2396
Exon: 2396-2449
Exon: 58311-58490
Exon: 58732-58785

Exon: 61383-61431
Exon: 61759-61824
Exon: 61914-61988
Exon: 62207-62259
Exon: 63025-63261
Exon: 63710-63829
Exon: 63931-64030
Exon: 64108-64220
Exon: 65353-65485
Exon: 65759-65937
Exon: 66216-66313
Exon: 67941-68198
Exon: 71417-71461
Exon: 72034-72391
Stop: 72392

Sim4 results:

Exon: 2396-2449, (Transcript Position: 1-54)
Exon: 58311-58490, (Transcript Position: 55-234)
Exon: 58732-58785, (Transcript Position: 235-288)
Exon: 61383-61431, (Transcript Position: 289-337)
Exon: 61759-61824, (Transcript Position: 338-403)
Exon: 61914-61988, (Transcript Position: 404-478)
Exon: 62207-62259, (Transcript Position: 479-531)
Exon: 63025-63261, (Transcript Position: 532-768)
Exon: 63710-63829, (Transcript Position: 769-888)
Exon: 63931-64030, (Transcript Position: 889-988)
Exon: 64108-64220, (Transcript Position: 989-1101)
Exon: 65353-65485, (Transcript Position: 1102-1234)
Exon: 65759-65937, (Transcript Position: 1235-1413)
Exon: 66216-66313, (Transcript Position: 1414-1511)
Exon: 67941-68198, (Transcript Position: 1512-1769)
Exon: 71417-71461, (Transcript Position: 1770-1814)
Exon: 72034-72394, (Transcript Position: 1815-2175)

CHROMOSOME MAP POSITION:
chromosome 11

ALLELIC VARIANTS (SNPs):

DNA

Position	Major	Minor	Domain
6469	A	G	Intron
10970	T	C	Intron
10977	T	C	Intron

FIGURE 3A-34

11044	T	A G C	Intron
11470	G	A	Intron
13050	T	G	Intron
13231	T	G	Intron
13813	C	G	Intron
28240	G	C	Intron
28472	G	T	Intron
36051	C	A	Intron
37118	A	G	Intron
46715	A	T	Intron
47190	G	A	Intron
50801	T	C	Intron
50877	-	A	Intron
53173	G	A	Intron
53756	G	A	Intron
55878	-	T	Intron
57192	A	C	Intron
57500	C	T	Intron
58984	C	A	Intron
59775	G	A	Intron
59869	T	G	Intron
59985	A	G	Intron
65094	G	A	Intron
73617	T	C	Intron
75055	T	A G C	Intron

Context:

DNA

Position

6469	TGGAGAAAGGTCCAGCTTCCAGAGTTCACCTGCTAGAGTTTTCCATAACACCTGGGGGAG AGGCTACTCCATCTGGGACCTGCCCCACCTCTGGGCCTCAGAACTATGAGAGAGGGATT GAGAGAAAACCTTGCCCCACTTCTGCTGCAGTGGGAAGGGAGGGGGCTGCTGTCAGGCTTC TAGGCAGTGAGCGGCATTGTTTATTCTCTCAGTTCAGGAAGGGGAGTTTAGAAGTACTG GTGAAGAAAACAAAGTTACAAGATCCTATAAGGAACAGCTGAACTACTCCAAACACTCTC [A,G] CTGGACCCCCATTGTTGATTCTGGATAAAAATATATATATATAAACTCTTTTTTTTTT TTGACACAGAGTCTTGCTCTGTGCGCCAGGCTGGAGTGTAGCGATGCGATCTCGGCTCAC TGCAACCTCCGCCTCCCGGTCAAGCGATTCTCCTGCCTCAGCCTCCTGGGAGTAGCTGG GACTACAGGCGCCCAACCACCATGCTGGCTAATTTTTGTATTTTGTAGAGACGGGGTTT TGCCATATTGGCCAAGCTGGTCTCGATCTCCTGACCTCAGGTGATCTGCTGGATAAATAT
10970	GACTCCCTTCCCAATTCAAACTTGGTGAAAGACCCTCAGCCTAGCCAGGAGGAAGGGAC TGGGTCTGCCTTTGGCTCCTCATTTATGGGTCTGGGAGGGGATCAGGACTCCTTACTGCT ATGATCTGGCTGCTAAATTCAGTGACATCCAGGCCTTTTTTCGTCCACGCAATGGGACT GTCTGTCCAGGCCTGCTGGGAAAGAAAAGAGAGAAAAAATAGTTTTTGCTCTTTGGCAGC

FIGURE 3A-35

TTACAGGGACTTCAGCCATAGGAAACAACCTGTAGGAAAGGTGGGAGCTTCCGGTCACCA
[T,C]
GTGTGCTGACACTTCCTGCAATAGCACTAGGGAGTCTTTCTCAGGGAGCAAGGCCAGCCA
GGTAGGATTATTTCCAGTCTCCAGCTAAGCAGGAAATGCCAAAATATGAACGTTTAGT
AATTAGTGAGTGTAACCTACCTGCTGACAGAGCTCCAGCCTAGACCTTGTCTTGGGGGCT
GGTTGCCCCTGTTGATACTACAGTGAGCTACTCATTGCTTCTGATTACCATTTTCAGTATG
AGTTTTGCTTTGGTTTCTGATATCCCATGTGCGGCTGCCTTTTTTCTCCACCTTCTTTTT

10977 TTCCCAATTCACAACCTGGTGAAAGACCCTCAGCCTAGCCAGGAGGAAGGGACTGGGTCT
GCCTTTGGCTCCTCATTTATGGGTCTGGGAGGGGATCAGGACTCCTTACTGCTATGATCT
GGCTGCTAAATTCAGTGACATCCCAGGCCTTTTTTCGTCCACGCAATGGGACTGTCTGTC
CAGGCCTGCTGGGAAAGAAAAGAGAGAAAAAATAGTTTTTGCTCTTTGGCAGCTTACAGG
GACTTCAGCCATAGGAAACAACCTGTAGGAAAGGTGGGAGCTTCCGGTCACCATGTGTGC
[T,C]
GACACTTCCTGCAATAGCACTAGGGAGTCTTTCTCAGGGAGCAAGGCCAGCCAGGTAGGA
TTATTTCCAGTCTCCAGCTAAGCAGGAAATGCCAAAATATGAACGTTTAGTAATTAGT
GAGTGTAACCTACCTGCTGACAGAGCTCCAGCCTAGACCTTGTCTTGGGGGCTGGTTGCC
CCTGTTGATACTACAGTGAGCTACTCATTGCTTCTGATTACCATTTTCAGTATGAGTTTTG
CTTTGGTTTCTGATATCCCATGTGCGGCTGCCTTTTTTCTCCACCTTCTTTTTGTTGTGT

11044 GTCCTCATTTATGGGTCTGGGAGGGGATCAGGACTCCTTACTGCTATGATCTGGCTGCT
AAATTCAGTGACATCCCAGGCCTTTTTTCGTCCACGCAATGGGACTGTCTGTCCAGGCCT
GCTGGGAAAGAAAAGAGAGAAAAAATAGTTTTTGCTCTTTGGCAGCTTACAGGGACTTCA
GCCATAGGAAACAACCTGTAGGAAAGGTGGGAGCTTCCGGTCACCATGTGTGCTGACACT
TCCTGCAATAGCACTAGGGAGTCTTTCTCAGGGAGCAAGGCCAGCCAGGTAGGATTATTT
[T,A,G,C]
CCAGTCTCCAGCTAAGCAGGAAATGCCAAAATATGAACGTTTAGTAATTAGTGAGTGTA
ACTACCTGCTGACAGAGCTCCAGCCTAGACCTTGTCTTGGGGGCTGGTTGCCCCTGTTG
ATACTACAGTGAGCTACTCATTGCTTCTGATTACCATTTTCAGTATGAGTTTTGCTTTGGT
TTCTGATATCCCATGTGCGGCTGCCTTTTTTCTCCACCTTCTTTTTGTTGTGTCTTTTTG
TTTTTTTGAGACGGAGTCTTGCTCTGTTGCCAGGCTGGAGTACAGTGGCACAATCTCAG

11470 ACAGTGAGCTACTCATTGCTTCTGATTACCATTTTCAGTATGAGTTTTGCTTTGGTTTCTG
ATATCCCATGTGCGGCTGCCTTTTTTCTCCACCTTCTTTTTGTTGTGTCTTTTTGTTTTT
TTGAGACGGAGTCTTGCTCTGTTGCCAGGCTGGAGTACAGTGGCACAATCTCAGCTCAC
TGCAACCTCCGCTTCCAGGTTCAAGCAATTCTGCCTTAGCCTCCCAAGTAGCTGGTACT
ACAGGCATGTGCCAGCACACCCGGCTAATTTTTTTTTTTTTTTTTTTTGAGACAGGGTCTC
[G,A]
CTCTGTGCCCAGGCTGGAGTGCACTGGCGGATCTCAGCTCACTGCAAGCTCTGCCTCC
CGGGTTACACCATTTCTCCTGCCTCAGCCTCCCGAGTAGCTGGGACTTCAGGCGCCCACC
ACCATGCCAGCTAATTTTTTTGTACTTTTTTTTTTTTTTAAAGTAGAGATGAGGTTTCACC
ATGTTAGCCAGGATGGTCTCAATCTCCTGACCTCATGATCCACCCACCTCGGCCTCCCAA
AGTGCTGGGATTACAGGCGTGAGCCACCGTGCCCGGCTGTAAACCTGGCTAATTTTTGT

13050 ATGGGAGAAGAATAGTACCCATCTTATAGGTATAGCTGTTATGAGTATTAAGAGATTAA
TGAATAGAAAGCATTTAGAATAGCGCCTGGCACAGCAGAATGATCATTGTATTATTGTT

FIGURE 3A-36

CCAGTTGAACAACACAGTGAATTTTATCTGAGCACCACAACTCTAGGTCAGTATAAGG
GGTGATGTTTGGGATTTCTCTGTAATCAGTTGAAAAAATCTTGTTCTGGCATCTTCAAGC
CACTGGGGTCTATAGGTGCTTTTTCTAACATTTCTGTTTTTTTGTGTTGTTGTTGTT
[T,G]
TTTGAGATGGAGTCTTGCTCTTGTTACCCAGGCTGGAGTGCAGTAGCACCATCTTGGCTC
ACTGTGACCTCCACCTCCCAGGTTCAAGCGATTCTCCTGCCTCAGCCTCCCAAGTAGCTG
GGATTACAGGCACCTGCCACCATACCTGGCTAATTTTTTTTTTTTTTTTTTTTTT
TATTTTTAGTAGAGATGGGGTTTACCATGTTGACCAGGCTGGTCTTGAACCTCTGACCT
CATGATCTGCCACCTCGGCCTCCCAAAGTGCTGGGATTACAGGCGTGAGCCACTGCACC

13231 GTGATGTTTGGGATTTCTCTGTAATCAGTTGAAAAAATCTTGTTCTGGCATCTTCAAGCC
ACTGGGGTCTATAGGTGCTTTTTCTAACATTTCTGTTTTTTTGTGTTGTTGTTGTTT
TTTGAGATGGAGTCTTGCTCTTGTTACCCAGGCTGGAGTGCAGTAGCACCATCTTGGCTC
ACTGTGACCTCCACCTCCCAGGTTCAAGCGATTCTCCTGCCTCAGCCTCCCAAGTAGCTG
GGATTACAGGCACCTGCCACCATACCTGGCTAATTTTTTTTTTTTTTTTTTTTTT
[T,G]
ATTTTTAGTAGAGATGGGGTTTACCATGTTGACCAGGCTGGTCTTGAACCTCTGACCTC
ATGATCTGCCACCTCGGCCTCCCAAAGTGCTGGGATTACAGGCGTGAGCCACTGCACCC
GCCCTAGTTTGCTTTTTTACCAATCACCTATCTGAAAAAATGGAATGCTACTGGAGAG
ATTCATGTACTTCTGAGAACACTTTTAGCTCATTTTTTATAAGGCATCAATATTAGATAG
TTTTCTTGATTAAAGAAAAAAAACACCACCCACTGCCTGCCTATATTTCTGGGTTGCAA

13813 CTATATTTCTGGGTTGCAAATGATGGCGGTGGATGTGCAGCCTCATCCGTGGCTAGAAGG
CCAAATCCAAAGTCACCAGAGCTTGAGTTTTTTGAGAGTTGAGATCTGTGTGTCAAAGGG
GAAGCCCTAGGGTGGTTCTCTGCAGCACCAGAGCAGGGATTACATACCATCATGTTCTT
TCTTTTTCTTTCTCGTCTTTCTTTCTTCTTTCTTTTGTCTCATGATTCTCACT
GTGTTGCCAGGCTGGTCTTGAATATTGGCCTCAAGTGATCCTCCCGCATTGGCCTCCC
[C,G]
AAGTGCTGGGATTACACACTCAGCCATGTTCTTTCTTCAAGTACGGTATTGACCTTTG
GCCACAGGAGAACGTGCCAGTTTTCTTAAAGACCACGTGGGAACCTCAGCAGCCCATGA
TTGTAGGTTCTTTTTCCCTCATAGAGTGGCCTTCAAGGGCAGGTTCTTGTTATCTGCGT
TTCAGAGACCCAAAGGGACACAGGCATTTCTGCTCCTGGGAATTTGCGGACTTTGAATCT
TGAGCTCAGATTTTGGTCTCTGTTGGTTGCTTGTTATCTTCATCTCTTGTCAATTTCTGG

28240 TATTAAATAAATAAATAAGATTTACTTATCCAAAAGCACAAATTATGTGCCTTTTTCTTT
TCTTTTGAGACGAGAGTCTGACTCTGTTGCCAGGCTGCTGTAGTACAGTGACGCAGTCT
C
[G,C]
GCCTTGACCTCCCAGGCTCAAGCAATCCTCCACCTCAGCCTCCCAAGTAGCTGGGACTA
CAGGCATGTGCCACTATGCCTGGCTAATTTTTTGCACTTTTTGTAGAGATGGGGTTTCGT
C

28472 TTTCTTTCTTTTGAGACGAGAGTCTGACTCTGTTGCCAGGCTGCTGTAGTACAGTGAC
GCAGTCTCGGCCTTGACCTCCCAGGCTCAAGCAATCCTCCACCTCAGCCTCCCAAGTAG
CTGGGACTACAGGCATGTGCCACTATGCCTGGCTAATTTTTTGCACTTTTTGTAGAGATG
GGGTTTCGTATGTTGCCAGGCTGGCCTGGAACCTCTGGCGTCAAGCAACCTACCTGCC

FIGURE 3A-37

TTCGCCTCCCAGAGTGCTGGGATTACAGGCAGTCGCCATTGTATCCAGCCCAGTTATGTA
[G,T]
TTATGTGCCATTTCTAAACTACTTTAGAACCCATCTCTTTGGTGTGTTGTTTGTGAGAC
AGAGTCTCACTCTGTCACCTCAGCTGGAGTGCAGTGGTGTGATCTCAGCTCACTGCAGCC
TCGGCCCCCAAGGTTCAAGCGACCCTCCACCTCAGCCTCCCAAGTAGCTGGGACCACAG
GTGCTCTTTTTGTAAAGAGTGGAAAAGCCAAGGTCCATGTACTTTTTTTGAGAAAGACAG
CCTGTTGGCTTTCTTCAGAGTGGTTCTGCCCTTCCCGTACCCCATCTCCAACACATTTT

36051 CTGCCCACCTCCTGCTATGTTCTAGTTCTGATAGGAGTACCATTCAAGTTCCTTGGCAGG
GGACCAACCCGCTTCTACCGTGGTTGGTTTCCCTCCTTTTCCCAGCTTGTTTGATGTGC
ACGTTCTCCAAAATCTTATGCAGCTGGTTGGCTCTGTAGTGCCCAGAGATTGGAGCTCC
TGCAACGGGAACCCCGCGCTTCCCTCCCTGGTTTATAGGGGCAGGGCTTGAAAATAAAGA
ATCATAATCTCCCTTCTCCTCCTCCTCCTCTCCCCACTTCTCCCTGCCCCACCCCCA
[C,A]
CCCCACCCCAACCTGCCAGGCAAACCTGGAGTGACCAGCTCAGAGCGGGACTCAGTCCAC
CTCCCTGCTCTGCATGTGAGCAGTGATCTGGAGGAGATTCCGGGGCGCATGAGTATGTGA
ACTCTGGAGCACGTTACTGTCCCGGGCTGGCACTCTGTGGCAGGTGTGTGCACTCATTCT
GCTGTTACTGGAGACCACTCTCCTTAGGGGTGATGGTGACCCAGCTAGATGTCTGCCAGG
TCTGTCCAAGGCCACCTGTTCTCTAATAGCTTGGGAAATGGAAAGCACTTCTAAATACC

37118 ACGGAGTCTTGCTCTGTTGCTCATGCTGGAGTGCAGTGGCGCGATCTCGGCTCGCTGCAA
CCTCCACACCCAGATTAAAGCGATTCTTCTGCCTCAGCCTCCCGAGTAGCTGAGACTGC
AGGCATGCGCCACCACGCCCAGCTAATTTTTGTATTTTAAATAAGAGACAGAGCTTCACC
ATGTTGGCCAGGCTGGTCTTGAACCTCCGAACTCAGGTGATCCGCCTGCCTCGGCCTCCC
GAGGGACTGGGATTACAGGCATGAGCTACTGTGCCCAGCCTGAAGATTGGTTATTTAGGG
[A,G]
CTGTGACAAATGGTTTTGTCAGAGGAGCACTGGAAAGCCTGTAACCTCACAGAGCCAGGGG
TCAGCTTTTGTGCCATAGCCTTATAGCTTCTGTGGCCTGTAGTGCCTGAGGCCAGGGGAT
CAGGTGCTGACCACCTTTCCCTCTTCTTCTGTGTCTTGCGGCCAGCGACTGTTATTGT
CAGGTTGACCCTCTGGTTAGAGAGGATGACTTTGGCCTGGTGTCCAGACTCCCTGCTGCC
TTATCCCCTCTGCCCTGGAACCTGCACCTAAAAACAATTACTTTCCTCCTGATTCCAACAT

46715 CACCATGTCATTCACTACTCCTCCTGCAGGATGGTTTTATGTTAGGAAAGAGGGTCCTC
TTTGCCTGATTGCCCAGCCATGGCAGAATTTGACTTTTCTTGTATAGAGGGAATACCA
GGATGACAGGAATCAACTTAGCTATACTGGTACTTACAGTCAAATTTCTAGGTATTGTAG
CTCTTCCCAGAGCCCAGAGAACCTTGGAGAGGGGAAACAATGGTTCTACCCAAAAATG
AAGCTAGATAATAATAGAATACATCATCAAGACATTACTGAACACCACGTTCTATGGTAA
[A,T]
CACTGACATGGATTTTCTTTTTTTTTTCTTTGAGACAGGGTCTTACTCTGTCACCCAG
GCTGGAGTGCAGCAGTGTGATCACGGCTCACTGCAGCCTCAGCCTACCTCCCTGGGCTCA
GGTGATCCTTCCACCTCAGCCTCCCAAGTAGCTGGGATTGCAGGCACTTGTCAACACACC
CCGGCTAATTTTTGTGTTTTTTGTAGAGCCTGTGTTTGCCATGTTGCCCAGGCTGGCC
TCGAGTTCCTAGGCTCAAGGGATCTGCCTGTCTTGGCCTCCCAAAGTGCTGGAATCAGAG

47190 CACACCCCGGCTAATTTTTGTGTTTTTTGTAGAGCCTGTGTTTTGCCATGTTGCCCAGG
CTGGCCTCGAGTTCCTAGGCTCAAGGGATCTGCCTGTCTTGGCCTCCCAAAGTGCTGGAA

FIGURE 3A-38

TCAGAGGTGTAAGCCACCACGCCCCGGCCAGATTTTCTCATTTAATCTTCACTCTAATTCT
GTGAAATGGGTACAGCTAGTATCTTTATGTCCCAAATGAGGAAACAGATTTGGAGAAGTT
ATGTCACCTTTGCTCATGTTCAGTCAGCTGGTAAGCAACAGAGGTGGGCAGAGCGACTATA
[G,A]

TAAGTTTTCTGTATAGTTTACCTCTTCTAAGTTTTCTGGAAGGCAGGAGCCAGATCGCACT
GAGCTTTGCAACTGGAGCCAGGGCTCCAGAGTACTGCTCAACAAAGGTTTGCTAGGGCAA
CAGTAGCTGGGGATTTAGCGACCAGACCCCAGCAAGCAGATTCTCAGGGATGAAAGTAGT
CCTGGAAGCCTCTAAAGCCCTGGTTGCTCAGTAGAATCTAGTTTCAAGAGGAGCCAGCA
TTTCAAGTGGCTCTGAAGACAGAGGAGATTTGGAGAGTGCTCTTTGCATTGTGGCTTCCA

50801 CTCTGAATGCCAATTTCTCAATGGAAAACAGGGAGACTACCTACCCTATAGGTCTGTGTT
TGGAGAAAACAAAGTGTAAGCGCTGGACATACAGTAGCATCAGAAATGCTGAATCCGTTG
GCCAGGGCTCATGTGTAAGGCAAACATTTCTTGGCCACTCCTGAGTAGCATGGTCTTGCA
GGAATATATGCTTAAGTGCTGTGAGAGCACAGAGGAAGCTTTGCCCTTCCCTAGAGGGTT
AATGGCTACCAACGTGAGAAGGTCACGGAGTTCCTTAATGAGAGGGAGCCTAGCCTAGAA
[T,C]

AGGGGATGAATGAGAAATTGTTCTGAGAACCAGAGGCAAGGCTGCAACCAGCACATAGAC
AGGGGTCGTTGGTCTAGAAGGGGAGTCTTCTCCAGATGAGAGACAGCCAGCTTGCCCTGT
GCTCACCATGTGCCCAGATAGTGGGGGCTTAGCAGGAGGAAGGTGTGAGGAATCCCAGGC
CTTTGGAATTCCTTGAGAAAGCAGTGTTGTTTTGAAGGTAAGGCAGGGGATTGGTGACTG
GAACTTGAGGTGAGTGAGAACCTAGGGATGAACGTTCAGAAGCAGGGCTGGAAGGAAC

50877 TAAGCGCTGGACATACAGTAGCATCAGAAATGCTGAATCCGTTGGCCAGGGCTCATGTGT
AAGGCAAACATTTCTTGGCCACTCCTGAGTAGCATGGTCTTGCAAGGAATATATGCTTAAG
TGCTGTGAGAGCACAGAGGAAGCTTTGCCCTTCCCTAGAGGGTTAATGGCTACCAACGTG
AGAAGGTCACGGAGTTCCTTAATGAGAGGGAGCCTAGCCTAGAATAGGGGATGAATGAGA
AATTGTTCTGAGAACCAGAGGCAAGGCTGCAACCAGCACATAGACAGGGGTCGTTGGTCT
[- ,A]

GAAGGGGAGTCTTCTCCAGATGAGAGACAGCCAGCTTGCCCTGTGCTCACCATGTGCCCA
GATAGTGGGGGCTTAGCAGGAGGAAGGTGTGAGGAATCCCAGGCCTTTGGAATTCCTTGA
GAAAGCAGTGTTGTTTTGAAGGTAAGGCAGGGGATTGGTGACTGGAACTTGAGGTGAG
TGAGAACCTAGGGATGAACGTTCAGAAGCAGGGCTGGAAGGAACTTAAAAGGGACATTTG
GATTGTTTCTAGCTTTTGGGCAAATCTAGGATTAATATGATTTTTTTCATTGATAGAAT

53173 GCTTAGTAACACTTGGTTTGCCTTTTGGTTCCAAATAACTGCCTTGCAAGGGTGACCCCT
TATTCTTTCTAAAGGCTACTTGAGAGCCATAGGGTCTACTCTTGACAGACCTCCTCCATC
CTTTAGGGCCTGTCTAGAGTATGATATAGGCCAGAGCTTTGGGAGTGCCTGGTGTGCCAC
GTCTTACTATAAGCAGGGAGGATGGTGGTAGAGGGGAGAGCGTGGCTTTTGCCAGGTCCT
ATTGAGTTGGCCCAGCAGGGCAGCTAATCCTCAGCCTGCCATCCTGTTGGTGAGACCCAG
[G,A]

GCCAAGCTGAATGGTGCAGCCAGAACCAAAAAGAGAACTCTCTCTCCATATTAGCCAC
TGCATACTCTTACCTCTTTATCCTTCAGGGAAGAAGCTAGGTGAGGAAGTTGCCTCACTT
GGGGCCTTGCCCAAGAAGCATTTCTGTTGGAGACTCTCTCCTCTTTTTCCCTTTTTCT
TTTCTCTGCTTCCTTCCAGTGGCTTGCCCTTACCCTGGCTCACATCCCTGCTGTGGGA
AACATCTTACAGCATAGAAGAAGGGGTGCAGGGGTAAAGTAAGGGAAGGATTGAGCACTTG

FIGURE 3A-39

53756

GGAAGGATTGAGCACTTGGAGTCCTCTGAGTTGGATGGTTCACTCCCGAAAAGGGGGTTG
GTGACTTTGGAGCAGGGGATCAAAGAGCAAGCACCAGTGCTTGTTGCTTCTCTGGCTCCT
GAACAAGCAGAACCTCCTCTCTTTCCCTGTCTGGATACCCAGCGTGGGACCAGCCCTTC
ACAGCCACCCTGTCTTGAGTTCCTGACTCTCCTCCTTCCCTCTTTGAAGGCTAGAGGTG
CTGGTGTGCGCTAGCAACAGGTTGAGGGAGTGTGGCATTTCACCAGGTCTGGAGGAGAGC
[G,A]
GGCACTCAACCTGGCCCCCTTCTGCGGAAAGGCCCGTAGCATCTCTTGTCAGCCTTCAGCT
GAGCTGTAGCTGGCTTAGCGGGCTCAACTTCGATTTGGAAGGTTGTTTTGACAGTGAGAC
TTCTGGATTGGCAGACAGTAGTATTTGGGGACATAATGATTGCTCTTATTGAACATCGGA
TAAGGCATTTTACATGTGCTCTTTCATCTACCTGTGTAAGTAGGGAATGTTTATTGCCA
CTTTACAGATAAGGAAATTAAAGCTTGACGTGGGGGAGCCAGGGCTTGAACCTGATTCT

55878

TCTAGGAATGCTGGACAGTTCCTTGGGTAGTAGCAAGTCATTCTTTTTTCTCTGTGGTT
TTTGAGTGCTTACGTACAGCCAGCAGGGGCCATGAAAGGAAGAACTTCACTCACACTC
CTCTGGTCACCCTGCTGCCCTCCAGACTGTTTCTTGAAGTTTCAAGGCAGCTCTGGAT
GGTTCTGGGATGAGGCTCTGGCCTCATATGCTTTGTTGCAGTATGCTGGAGCGATCGCTC
CAGATGTTCTTTGTGAGATGTAAACCAGGGCGCTAATCAGGAGTTAGACCAGACTCTGCA
[-,T]
TTTTTTTTTTTTTTTTTGGAGACAGGGTCTCGCTCTATCACCCAGGCTGGAGTACAATGG
CATGATCATGGCTCACTGCAGCCTCGAACTCCTCCTGGGTCAAGCGATCCTCCCGCCTC
ATCCTCCAGAGCAGCTGGGACTATAGGTGCATGCCACCACACCCAGTTGATTTCTTAATT
TTTTTTTTTTTTTTTTTGGAGACGGAGTTTCACTCTTGTTGCCAGGCTGGAGTGCAGT
GGTGGCATCTCAGCTCACTGTAACTCCTCCTCCTGGGTCAAGCAATTCTCCTGCCTCA

57192

CCACAAGTGGAATTTCTACACGTAACCCCATATGACAGGTTATAAGCAAAATTCATCA
CTTTATTTTCATGCACAAAATTTATTTTAAATGTATGAAATTTACCTTCAGGCCATGTATA
TAATGTACACATGAAAAATAAATGTTTAGACTTGGGTCCCATCCCTGAGATATCTGATTA
TGTATATGCAAATATTCCAAAATCCAAAACAATTTAAATCTGCCAGTTTCTGGTCCTA
AGCATTTTGGATAAAGGATATTCAACCCGTATTATGTTTATATGCCTCTTCAGTGCTGGT
[A,C]
GTTGTAGCTTCTGCTTCTCATCCCTCATTTGAGCCGGGTGGCAGAGCAGGGCAGACTG
CTGCCTTGCTCAGACCTAATCGTTCAGTTCTTTCATTGTACAAGTATTCATTGAGCAGCA
AACATAAGCCAGTCTCTCTAAGTGCTGGGATGTATCAGTGAATAAAGAATATATGCCTGC
TTTCATGTGCTTCCATTTTACTGGGGGAGATGGCAAATAAATGTAAAGTGATAAATAAC
AAAGGTTCAGTGGGGCATTCTAGTTCAGCGGCAGAAATTTCTGTCCTACGCGGGAGAC

57500

CTTCTGCTTCTCATCCCTCATTTGAGCCGGGTGGCAGAGCAGGGCAGACTGCTGCCTT
GCTCAGACCTAATCGTTCAGTTCTTTTATTGTACAAGTATTCATTGAGCAGCAAACATAA
GCCAGTCTCTAAGTGCTGGGATGTATCAGTGAATAAAGAATATATGCCTGCTTTCATG
TGCTTCCATTTTACTGGGGGAGATGGCAAATAAATGTAAAGTGATAAATAACAAAGGT
CAGTGGGGCATTCTAGTTCAGCGGCAGAAATTTCTGTCCTACGCGGGAGACTCGGGTT
[C,T]
GACTTCGGCCATGCAGTCCTTCCATGCAGGAAGGGCTACTACGTTTCTACCCAACAAAGT
TATTATGGCTGGACGCAGTGGCTCACGCCTGTAATTCAGCACTTTGGGAGGCCAAGGCC
GGCGGATCACCTGAGATCAGGAGTTTGAGACCAGCCTGACCAACATGGAGAAACCTATC
TCTATTGAAAATACAAAATTAGCCAGGCGTGGTGGCGCATGACTGTAATCCAGCTACTC

FIGURE 3A-40

GGGAGGCTGAGGTGGGAGAATTGCTTGAACCCGGGAGGTGGAGGTTGCGGTGAGCTGAGA

58984 TTTGCTGGTCAGAGAAGTGATTTGGGGCCTTTTGTCTCATCCTCAGGTAGCTGTGAAG
ATCATTGACAAGACTCAACTGAACTCCTCCAGCCTCCAGAAAGTAAGCACATGGCACCTC
CTGTCCCTTTTTTTTTTTTTTTTTTTTTTTTTTTTGTGAGTCAGAGCCTCACTCTTGTGCCCC
AGGCTGGAGTGCAATGGTGTGATCTCGGCTCACTGCAACCTCCGCCTTTGGTTTCAAGC
GATTCTCCCGCCTCAGCCTCCCGAGTAGCTGGGATTATAGGCACCCGCCACACACCTGG
[C,A]
TAAGTTTTGTATTTTAGTAGAGATGGGGTTTACCATGGTAGCCAGGCTGGTCTCGAAC
TCCTGACCTCAAGTGATCCGCTCGCCTCGGCCTCCCAAAGTGCTAGGATTATAGGCGTGA
ACCACTGCCCCCAGCCCACCTGTCCCTTCTAAATCTCTTCTGGGGTCAATGATCTAC
TGACCCCATTTAGACCTTCTTTGAATTCCTAGTTTAAATTTCTGGCCATTTGCTCAC
GTCCCCCAACCATTCCCTCCCATGGCTCTGCTACCTTCGGGGCTTTGGTTGGATCATCT

59775 AGATCTGGAATGATACAGGGGAGTGGCTTTAGAAATACAAGAATAAGAGGAAGCAGGGAA
CCTGCCGGTGGGTTCTGTGCCAGCTACCTTTAGAGAATGAGCTCCAGCTCAAATTTTCT
GAACAAAACCTAGTTCTGTTTCATCTTGTGGCAAATCAGATATTTTCTCCATAAGCATATT
GTGGCAGTTGAGTTAGGAGAAGGCATGATTCTGTGCTAACAGAGTCAGATAGTGATACTGG
GAACCTTAGGAGTAAGGGCTGAGGATTGTTGTTGAGGGCGATGCTCATGGAATTAGAGTG
[G,A]
ATGAGTTGTTCTCCGGACATGCAAATAGCCAGAACCAAGGTGTTTCCTATTTATTGTTAC
CCCTGGGATCCCTTCAAGGGTCTTCAGTTGAGTAGAAACATTGTTGTCATCATCAGGGT
GTCTCTGCTTGAAGCTTTCCAGGAGGAAGGGAAAAAGGGCTGCTTATGACATCCTGGCTC
CAGCCCCACAGAAGAAGTCAGCGTGGGGTAGGCCATTTGGCCTTGGGAGCAGTCTAGCCT
GCCATCGTAATAATCGCCAGTCCACCAAGCCATCTTATTCCTGACCTTGTTTTCTCCCT

59869 AGAATGAGCTCCAGCTCAAATTTTCTGAACAAAACCTAGTTCTGTTTCATCTTGTGGCAA
TCAGATATTTTCTCCATAAGCATATTGTGGCAGTTGAGTTAGGAGAAGGCATGATTCTGTG
CTAACAGAGTCAGATAGTGATACTGGGAACCTTAGGAGTAAGGGCTGAGGATTGTTGTTG
AGGGCGATGCTCATGGAATTAGAGTGGATGAGTTGTTCTCCGGACATGCAAATAGCCAGA
ACCAAGGTGTTTCCTATTTATTGTTACCCCTGGGATCCCTTCAAGGGTCTTCAGTTGAG
[T,G]
AGAAACATTGTTGTCATCATCAGGGTGTCTCTGCTTGAAGCTTTCCAGGAGGAAGGGAAA
AAGGGCTGCTTATGACATCCTGGCTCCAGCCCCACAGAAGAAGTCAGCGTGGGGTAGGCC
ATTTGGCCTTGGGAGCAGTCTAGCCTGCCATCGTAATAATCGCCAGTCCACCAAGCCATC
TTATTCCTGACCTTGTTTTCTCCCTAATTCTTCTGGTTTTCTCCCTAATTCTTCTGAG
CTCTCTGGAAGGCACCAACACCAGACAAATAGAGCCATTTTCAAACCTTTGAGACTCT

59985 CGTGCTAACAGAGTCAGATAGTGATACTGGGAACCTTAGGAGTAAGGGCTGAGGATTGTT
GTTGAGGGCGATGCTCATGGAATTAGAGTGGATGAGTTGTTCTCCGGACATGCAAATAGC
CAGAACCAAGGTGTTTCCTATTTATTGTTACCCCTGGGATCCCTTCAAGGGTCTTCAGT
TCAGTAGAAACATTGTTGTCATCATCAGGGTGTCTCTGCTTGAAGCTTTCCAGGAGGAAG
GGAAAAAGGGCTGCTTATGACATCCTGGCTCCAGCCCCACAGAAGAAGTCAGCGTGGGGT
[A,G]
GGCCATTTGGCCTTGGGAGCAGTCTAGCCTGCCATCGTAATAATCGCCAGTCCACCAAGC
CATCTTATTCCTGACCTTGTTTTCTCCCTAATTCTTCTGGTTTTCTCCCTAATTCTTC

FIGURE 3A-41

CTGACTCTCTGGAAGGCACCAACACCAGACAAATAGAGCCATTTTCAAAACCTTTTGAGA
CTCTTTGTTACTAAAGCCAGTCTGATTCTGGCCAAAAATGTGATCTCAGCAATGATCCCT
GAAAAATGAACATTGAAGAAGCTAGCCCCCTCAGGGGTCTAGACAAGCCCAGAAAACCCC

65094

CGGCTATTGAGTCTGTTGCTTCTGTCTAGTGCTTTATGTTTGGGTGTGTGTATCTGTGTG
TGTGTGTGTGTGTGTGTGTGTGTGTATGTGTCCGCTTCCCCTGTGTGGATCTGGAGACT
TTGTGATTGTTCTTCTGCCCATTTGGGTTTTGTTTCATCATCTGAGTATCCCCACATGAAC
TCCCAGCCTCCCTGCCCTGCTCTCCCTCTGGTGGTGGGATCCTTAAGAGGCACCTGGTGA
CACTTGGTATAGGCCCATATTGCTCTGTGTTGAGGGGAGTGGACTTGAGTCTGGACATGT
[G,A]

TTCTTGCGGATGTTTGTGTCTCTGGGTGTGTGGGCTTATGTATTCTTTCTGAGACTGTG
TTTGTCA GTGTCTGTGTCA GAGCATGTGTGTCTCCAGGGTCTCTCCAGGGGGGATGTAT
TGGTCTTACAAGTGGATGTCCGGTATGATCCTGGGGTGTTTGAGTGTTGGGAGAGGGCGG
TATGTGTA AATGTGTCCATCCATAGGGATCTCCACATGACTTCTGCCCTCCCTTGAAGCT
GTTTTCTGTTTCTTTCAGCTGGAAGGCGACACCATCACCCTGAAACCCCGGCCCTTCAGCT

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ACTGGGCACTCTGTGATGGGGGAGCCTTTGTCTGAAAGCACAGCCCTCGCCCTTCCTC
TCCCCATGGCTTCCCCTTCATTGGCATTAACTCTGGGCACCAGCTCTCTCCATAGCAGTGA
CTTCCCTCACCCTCTCATCTCTCAGCCTTGCCCTTTTCTTCCTGACACTGTGCCCCCTC
CTCTCAGGAGACACTGCCGAGGGCCACCTGGCAGAAGGCTGAGTTAGGCAGCAGGGCCGG
GAGCGTCTGCCCTCCACAGGGTGGGGGACAGATAGGCTAAGCGACTCCAGCTTGCTACC
[T,C]

TCAGTGGCCAGTGTGGGCGTGGGCGGTTTGGGGCGCTTGGCTGGTGGTGGCCACTGCATC
CCTTAATTTATTTCTCTGCTGTTTCTGTTCTTGAGAAATTGGGGGTGGGAGTCCTACACA
GAGGCTGCCCCACCTCACCTGAGTTGTACATTTTTTTGTGATGGGTTTTATTTTTTAT
TATTTTATTTTATTTTTTTTTTTTTTTGATTTATGATGACTCCACCCCTCTTCATCACCC
CCGCTCCCAGGCCAGGCTCAGCGATTAAGCCGAGCCCTTGCCTCCTAGGAAGGGGCGCTTG

75055

GACACAGCCATTCCAGTACCGGCCAGGAAGCGAAAGTGCCCTCAGGCCAGCTCAAAGGCC
CCTGAGCCC GGCCATGGCCCCAGGAGACAGGCCAGCTGCCAGGAACATGCAGAACCC
AAAGGGCGGGGCTGGGCTGTCCGAACTCTGGTCTTACAAAGACCCCGCCAGAGCCCTAG
TCCCTTCTGTCTCAGTGACACCAGAGATGCCTGGGGATGGCCAGCAAAGGGGTCTTGGA
GCCCCGTGTTGGTGGAGGACGTCAGGGCTCAGAGTGAGGGTGCTGGGGGCTCCAGAGGGG
[T,A,G,C]

TCCAATCAGGGTGGGTGGGGGCTGAGGGCCAGGGCGGGCGCTGTGGCGGGGGGCAGCCAG
AGCGGGGCGGATGAGAGGCGGTGGGGGCTGTTGGGGGCCAGCCGGGGCTGGAGGAAGCG
GCCCTGCTGCAGTGGGGGTGGCTGTCGAGCAGAGTGGGAGCCGTGGGCAAAGGTGGCCT
CAGCAGCGGGGGTGGCTGGGACAGCGAGGTGGGAGGTGGAGGGGGTGGTGGCGCAGGGGG
CACTGATCGGGGCACGGACGTGGAGACCGATGTAATCTGGACCTGAGGGGAGAGGAAAGA